

TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371

1781-0163P

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

09/913898

INTERNATIONAL APPLICATION NO.

PAC/SG99/00079

INTERNATIONAL FILING DATE

July 16, 1999

PRIORITY DATE CLAIMED

February 18, 1999

TITLE OF INVENTION

CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT TRANSGENIC ORNAMENTAL FISH

APPLICANT(S) FOR DO/EO/US

GONG, Zhiyuan; HE, Jiangyan; JU, Bensheng; LAM, Toong Jin; XU, Yanfei; YAN, Tie

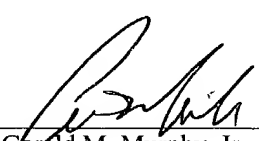
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39 (1).
4. ☐ The US has been elected by the expiration of 19 months from the priority date (Article 31).
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau. WO 00/49150
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☒ An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)).
 - a. ☒ is transmitted herewith.
 - b. ☐ has been previously submitted under 35 U.S.C. 154(d)(4)
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ An English language translation of the annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 20. below concern document(s) or information included:

11. ☒ An Information Disclosure Statement under 37 CFR 1.97 and 1.98./International Search Report (PCT/ISA/210).
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.
14. ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
15. ☐ A substitute specification.
16. ☐ A change of power of attorney and/or address letter.
17. ☐ A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 and 35 U.S.C. 1.821-1.825.
18. ☐ A second copy of the published international application under 35 U.S.C. 154(d)(4).
19. ☐ A second copy of the English language translation of the international application under 35 U.S.C. 154(d)(4).
20. ☒ Other items or information:
PCT/IPEA/409
Fifteen (15) sheets of formal drawings

518 Rec CT/PTO 17 AUG 2001

U.S. APPLICATION NO. (if known, see 37 CFR 1.5)		INTERNATIONAL APPLICATION NO.		ATTORNEY'S DOCKET NUMBER	
09/913898		PCT/SG99/00079		1781-0163P	
21. <input checked="" type="checkbox"/> The following fees are submitted:				CALCULATIONS PTO USE ONLY	
BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO. \$1,000.00					
International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$860.00					
International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO. \$710.00					
International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$690.00					
International preliminary examination fee (37 CFR 1.482) paid to USPTO and all claims satisfied provisions of PCT Article 33(1)-(4). \$100.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$	1,000.00
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input checked="" type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				\$	130.00
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total Claims	39 - 20 =	19	X \$18.00	\$	342.00
Independent Claims	8 - 3 =	5	X \$80.00	\$	400.00
MULTIPLE DEPENDENT CLAIM(S) (if applicable) Yes			+ \$270.00	\$	270.00
TOTAL OF ABOVE CALCULATIONS =				\$	2,142.00
<input checked="" type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.				\$	-1,071.00
SUBTOTAL =				\$	1,071.00
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).				\$	0.00
TOTAL NATIONAL FEE =				\$	1,071.00
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property +				\$	0.00
TOTAL FEES ENCLOSED =				\$	1,071.00
				Amount to be: refunded	\$
				charged	\$
a. <input checked="" type="checkbox"/> A check in the amount of \$ <u>1,071.00</u> to cover the above fees is enclosed.					
b. <input type="checkbox"/> Please charge my Deposit Account. No. _____ in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed.					
c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>02-2448</u> .					
NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.					
Send all correspondence to: Birch, Stewart, Kolasch & Birch, LLP or Customer No. 2292 P.O. Box 747 Falls Church, VA 22040-0747 (703)205-8000					
Date: <u>August 17, 2001</u>					
By  #32568 Gerald M. Murphy, Jr., #28,977					

/REM

09/913898
518 RES PCT/PTO 17 AUG 2001

PATENT
1781-0163P

IN THE U.S. PATENT AND TRADEMARK OFFICE

Applicant: GOGN, Zhiyuan et al. Conf.:
Int'l. Appl. No.: PCT/SG99/00079
Appl. No.: New Group:
Filed: August 17, 2001 Examiner:
For: CHIMERIC GENE CONSTRUCTS FOR
GENERATION OF FLUORESCENT
TRANSGENIC ORNAMENTAL FISH

PRELIMINARY AMENDMENT

BOX PATENT APPLICATION

Assistant Commissioner for Patents
Washington, DC 20231

August 17, 2001

Sir:

The following Preliminary Amendments and Remarks are respectfully submitted in connection with the above-identified application.

AMENDMENTS

IN THE SPECIFICATION:

Please amend the specification as follows:

Before line 1, insert --This application is the national phase under 35 U.S.C. § 371 of PCT International Application No. PCT/SG99/00079 which has an International filing date of July 16, 1999, which designated the United States of America and was published in English.--

Docket No. 1781-0163P

REMARKS

The specification has been amended to provide a cross-reference to the previously filed International Application.

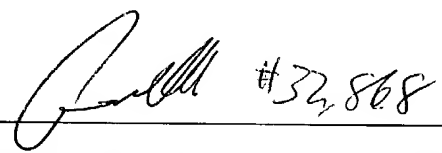
Entry of the above amendments is earnestly solicited. An early and favorable first action on the merits is earnestly solicited.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,

BIRCH, STEWART, KOLASCH & BIRCH, LLP

By

 #32,868
for Gerald M. Murphy, Jr., #28,977

P.O. Box 747

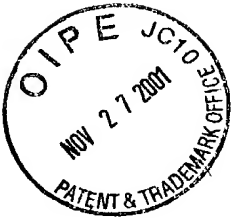
Falls Church, VA 22040-0747

(703) 205-8000

GMM/rem

1781-0163P

Attachment:



BOX SEQUENCE
PATENT
1781-0163P

IN THE U.S. PATENT AND TRADEMARK OFFICE

Applicant:	GONG et al.	Conf.:	5940
Appl. No.:	09/913,898	Group:	To Be Assigned
Filed:	August 17, 2001	Examiner:	TO BE ASSIGNED
For:	CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT TRANSGENIC ORNAMENTAL FISH		

AMENDMENT

Assistant Commissioner for Patents
Washington, DC 20231

November 27, 2001

Sir:

In response to the Notification of Missing Requirements Under 35 U.S.C. 371 in the United States Designated/Elected Office (DO/EO/US) mailed October 30, 2001, the following amendments and remarks are respectfully submitted in connection with the above-identified application.

In the Specification:

Please delete pages 24-46 of the specification containing the Sequence Listing. Please renumber the remaining pages of the specification, beginning with the "References", consecutively from

page 24. Please insert the Substitute Sequence Listing enclosed herewith immediately after the abstract.

In the References:

Please renumber the pages containing the references, pages 47-51, to 24-28, respectfully.

In the Claims:

Please renumber the pages containing the claims, pages 52-53, to 29-30, respectfully.

In the Abstract:

Please renumber the page containing the abstract, page 54, to 31.

REMARKS

Enclosed herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a Substitute Sequence Listing to be inserted into the specification as indicated above. The Substitute Sequence Listing in no way introduces new matter into the specification. Also submitted herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a disk copy of the Substitute Sequence Listing. The disk copy

Docket No. 1781-0163P

of the Sequence Listing, file "2001-11-12 1781-163P.txt", is identical to the paper copy, except that it lacks formatting.

The amendments to the Specification, References, Claims, and Abstract are merely to correct page numbers. No new matter is introduced by these amendments.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,
BIRCH, STEWART, KOLASCH & BIRCH, LLP

By Theresa A. Rupert #45702
for Gerald M. Murphy, Jr., #28,977
P.O. Box 747
Falls Church, VA 22040-0747
(703) 205-8000

GMM/LPS

Attachments: Disk Copy of Substitute Sequence Listing
 Paper Copy of Substitute Sequence Listing
 Copy of Notification

(Rev. 03/27/01)

SEQUENCE LISTING



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 LAM, Toong Jin
 JU, Bensheng
 XU, Yanfei
 HE, Jiangyan
 YAN, Tie

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 TRANSGENIC ORNAMENTAL FISH

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Val Glu Lys Leu Ser Val Glu Ala Leu Ser Ser Leu Asp Gly Glu Phe			
155	160	165	
aag ggc aag tac tac ccc ctg aag tcc atg act gat gac gag cag gag			640
Lys Gly Lys Tyr Tyr Pro Leu Lys Ser Met Thr Asp Asp Glu Gln Glu			
170	175	180	185
cag ctg atc gct gac cac ttc ctc ttt gac aaa ccc gtc tcc ccc ctg			688
Gln Leu Ile Ala Asp His Phe Leu Phe Asp Lys Pro Val Ser Pro Leu			
190	195	200	
ctg ctg gct gct ggt atg gcc cgt gac tgg ccc gat gcc aga ggc att			736
Leu Leu Ala Ala Gly Met Ala Arg Asp Trp Pro Asp Ala Arg Gly Ile			
205	210	215	
tgg cac aat gag aac aaa gcc ttc ctg gtc tgg gtg aaa cag gag gat			784
Trp His Asn Glu Asn Lys Ala Phe Leu Val Trp Val Lys Gln Glu Asp			
220	225	230	
cac ctg cgt gtc att tcc atg cag aag ggt ggc aac atg aag gaa gtg			832
His Leu Arg Val Ile Ser Met Gln Lys Gly Gly Asn Met Lys Glu Val			
235	240	245	
ttc aag cgc ttc tgc gtt ggt ctt cag agg att gag gaa att ttc aag			880
Phe Lys Arg Phe Cys Val Gly Leu Gln Arg Ile Glu Glu Ile Phe Lys			
250	255	260	265
aag cac aac cat ggg ttc atg tgg aac gag cat ctt ggt ttc gtc ctg			928
Lys His Asn His Gly Phe Met Trp Asn Glu His Leu Gly Phe Val Leu			
270	275	280	
acc tgc ccc tcc aac ctg ggc aca ggc ctg cgc ggt gga gtc cac gtc			976
Thr Cys Pro Ser Asn Leu Gly Thr Gly Leu Arg Gly Gly Val His Val			
285	290	295	

aag ctg ccc aag ctc agc aca cat gcc aag ttt gag gag atc ctg acc 1024
 Lys Leu Pro Lys Leu Ser Thr His Ala Lys Phe Glu Glu Ile Leu Thr
 300 305 310

aga ctg cgc ctg cag aag cgt ggc aca ggg ggt gtg gac acc gct tcc 1072
 Arg Leu Arg Leu Gln Lys Arg Gly Thr Gly Gly Val Asp Thr Ala Ser
 315 320 325

gtt ggt gga gtg ttt gac att tcc aac gct gac cgt atc ggc tct tca 1120
 Val Gly Gly Val Phe Asp Ile Ser Asn Ala Asp Arg Ile Gly Ser Ser
 330 335 340 345

gag gtt gag cag gtg cag tgt gtg gtt gat ggt gtc aag ctg atg gtg 1168
 Glu Val Glu Gln Val Gln Cys Val Val Asp Gly Val Lys Leu Met Val
 350 355 360

gag atg gag aag aag ctg gga gaa ggc cag tcc atc gac agc atg atc 1216
 Glu Met Glu Lys Lys Leu Gly Glu Gly Gln Ser Ile Asp Ser Met Ile
 365 370 375

cct gcc cag aag taa agcgggagggc ccttccattt ttttcttcgt ctttgtctgt 1271
 Pro Ala Gln Lys
 380

ttttttacag tccaacagca acgsagagga aaactgctgc tcaaaaagac agtctcacct 1331
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 aaaaaaaaaa aaaaaaaaaa 1589

<210> 4
 <211> 381
 <212> PRT
 <213> Danio rerio

<400> 4
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Val Leu Thr Lys Glu Met Tyr Gly Lys Leu Arg Asp Lys Gln Thr Pro
 35 40 45

Pro Gly Phe Thr Val Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro
 50 55 60

Gly His Pro Phe Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu
 65 70 75 80

Ser Tyr Asp Val Phe Lys Asp Leu Phe Asp Pro Val Ile Ser Asp Arg
 85 90 95

His Gly Gly Tyr Lys Ala Thr Asp Lys His Lys Thr Asp Leu Asn Phe
 100 105 110
 Glu Asn Leu Lys Gly Gly Asp Asp Leu Asp Pro Asn Tyr Phe Leu Ser
 115 120 125
 Ser Arg Val Arg Thr Gly Arg Ser Ile Lys Gly Tyr Pro Leu Pro Pro
 130 135 140
 His Asn Ser Arg Gly Glu Arg Arg Ala Val Glu Lys Leu Ser Val Glu
 145 150 155 160
 Ala Leu Ser Ser Leu Asp Gly Glu Phe Lys Gly Lys Tyr Tyr Pro Leu
 165 170 175
 Lys Ser Met Thr Asp Asp Glu Gln Glu Gln Leu Ile Ala Asp His Phe
 180 185 190
 Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Leu Ala Ala Gly Met Ala
 195 200 205
 Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Glu Asn Lys Ala
 210 215 220
 Phe Leu Val Trp Val Lys Gln Glu Asp His Leu Arg Val Ile Ser Met
 225 230 235 240
 Gln Lys Gly Gly Asn Met Lys Glu Val Phe Lys Arg Phe Cys Val Gly
 245 250 255
 Leu Gln Arg Ile Glu Glu Ile Phe Lys Lys His Asn His Gly Phe Met
 260 265 270
 Trp Asn Glu His Leu Gly Phe Val Leu Thr Cys Pro Ser Asn Leu Gly
 275 280 285
 Thr Gly Leu Arg Gly Gly Val His Val Lys Leu Pro Lys Leu Ser Thr
 290 295 300
 His Ala Lys Phe Glu Glu Ile Leu Thr Arg Leu Arg Leu Gln Lys Arg
 305 310 315 320
 Gly Thr Gly Gly Val Asp Thr Ala Ser Val Gly Gly Val Phe Asp Ile
 325 330 335
 Ser Asn Ala Asp Arg Ile Gly Ser Ser Glu Val Glu Gln Val Gln Cys
 340 345 350
 Val Val Asp Gly Val Lys Leu Met Val Glu Met Glu Lys Lys Leu Gly
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 Glu Gly Gln Ser Ile Asp Ser Met Ile Pro Ala Gln Lys
 370 375 380

<210> 5

<211> 1104
 <212> DNA
 <213> Danio rerio

<220>
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 <222> (75)..(1034)

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 <222> (45)..(64)
 <223> ARP2

<220>
 <221> primer_bind
 <222> (87)..(112)
 <223> ARP1

<220>
 <221> polyA_signal
 <222> (1069)..(1074)

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 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn
 1 5 10
 tat ttt ctg aaa atc atc caa ctg ctg gat gac ttc ccc aag tgt ttc 158
 Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe
 15 20 25
 atc gtg ggc gca gac aat gtc ggc tcc aag cag atg cag acc atc cgt 206
 Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg
 30 35 40
 ctg tcc ctg cgg ggc aag gcc gtc gtg ctc atg ggg aaa aac acc atg 254
 Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met
 45 50 55 60
 atg agg aag gcc att cgt ggc cac ctg gaa aac aac cca gct ctg gag 302
 Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu
 65 70 75
 agg ctg ctt ccc cac atc cgc ggc aac gtg ggc ttc gtc ttc acc aag 350
 Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys
 80 85 90
 gag gat ctg act gag gtc cga gac ctg ctg ctg gca aac aaa gtg ccc 398
 Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro
 95 100 105
 gct gct gcc cgt gct ggt gcc atc gcc ccc tgt gag gtg act gtg cgg 446
 Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro
 110 115 120

gcc cag aac acc ggg ctc ggt cct gag aag acc tct ttc ttc cag gct 494
 Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala
 125 130 135 140

ttg gga atc acc acc aag atc tcc aga gga acc att gaa atc ttg agt 542
 Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser
 145 150 155

gac gtt cag ctt atc aaa cct gga gac aag gtg ggc gcc agc gag gcc 590
 Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala
 160 165 170

acg ctg ctg aac atg ctg aac atg ctg aac atc tgc ccc ttc tcc tac 638
 Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr
 175 180 185

ggg ctg atc atc cag cag gtg tat gat aac ggc agt gtc tac agc ccc 686
 Gly Leu Ile Ile Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro
 190 195 200

gag gtg ctg gac atc act gag gac gcc ctg cac aag agg ttc ctg aag 734
 Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys
 205 210 215 220

ggt gtg agg aac atc gcc agt gtg tgt ctg cag atc ggc tac cca act 782
 Gly Val Arg Asn Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr
 225 230 235

ctt gct tcc atc cct cac act atc atc aat gga tac aag agg gtc ctg 830
 Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu
 240 245 250

gct gtc act gtc gaa aca gac tac aca ttc ccc ttg gct gag aag gtg 878
 Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val
 255 260 265

aag gcc tac ctg gct gat ccc acc gct ttc gct gtt gca gcc cct gtt 926
 Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val
 270 275 280

gcg gca gct aca gag cag aaa tcc gct gct cct gcg gct aaa gag gag 974
 Ala Ala Ala Thr Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu
 285 290 295 300

gca ccc aag gag gat tct gag gag tct gat gaa gac atg ggc ttc ggc 1022
 Ala Pro Lys Glu Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly
 305 310 315

ctg ttt gat taa accagacacc gaatatccat gtctgttttaa catcaataaa 1074
 Leu Phe Asp

acatctggaa acaaaaaaaaaa aaaaaaaaaa 1104

<210> 6
 <211> 319
 <212> PRT

<213> Danio rerio

<400> 6

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			20					25					30		
Asp	Asn	Val	Gly	Ser	Lys	Gln	Met	Gln	Thr	Ile	Arg	Leu	Ser	Leu	Arg
		35					40					45			
Gly	Lys	Ala	Val	Val	Leu	Met	Gly	Lys	Asn	Thr	Met	Met	Arg	Lys	Ala
	50					55					60				
Ile	Arg	Gly	His	Leu	Glu	Asn	Asn	Pro	Ala	Leu	Glu	Arg	Leu	Leu	Pro
65					70					75					80
His	Ile	Arg	Gly	Asn	Val	Gly	Phe	Val	Phe	Thr	Lys	Glu	Asp	Leu	Thr
				85					90					95	
Glu	Val	Arg	Asp	Leu	Leu	Leu	Ala	Asn	Lys	Val	Pro	Ala	Ala	Ala	Arg
			100					105					110		
Ala	Gly	Ala	Ile	Ala	Pro	Cys	Glu	Val	Thr	Val	Pro	Ala	Gln	Asn	Thr
		115					120						125		
Gly	Leu	Gly	Pro	Glu	Lys	Thr	Ser	Phe	Phe	Gln	Ala	Leu	Gly	Ile	Thr
	130					135						140			
Thr	Lys	Ile	Ser	Arg	Gly	Thr	Ile	Glu	Ile	Leu	Ser	Asp	Val	Gln	Leu
145					150					155					160
Ile	Lys	Pro	Gly	Asp	Lys	Val	Gly	Ala	Ser	Glu	Ala	Thr	Leu	Leu	Asn
				165					170					175	
Met	Leu	Asn	Met	Leu	Asn	Ile	Ser	Pro	Phe	Ser	Tyr	Gly	Leu	Ile	Ile
		180						185					190		
Gln	Gln	Val	Tyr	Asp	Asn	Gly	Ser	Val	Tyr	Ser	Pro	Glu	Val	Leu	Asp
		195					200					205			
Ile	Thr	Glu	Asp	Ala	Leu	His	Lys	Arg	Phe	Leu	Lys	Gly	Val	Arg	Asn
	210					215					220				
Ile	Ala	Ser	Val	Cys	Leu	Gln	Ile	Gly	Tyr	Pro	Thr	Leu	Ala	Ser	Ile
225					230					235					240
Pro	His	Thr	Ile	Ile	Asn	Gly	Tyr	Lys	Arg	Val	Leu	Ala	Val	Thr	Val
				245					250					255	
Glu	Thr	Asp	Tyr	Thr	Phe	Pro	Leu	Ala	Glu	Lys	Val	Lys	Ala	Tyr	Leu
		260						265					270		
Ala	Asp	Pro	Thr	Ala	Phe	Ala	Val	Ala	Ala	Pro	Val	Ala	Ala	Ala	Thr
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Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu
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Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
305 310 315

<210> 7
<211> 2241
<212> DNA
<213> Danio rerio

<220>
<221> TATA_signal
<222> (2103)..(2108)

<220>
<221> primer_bind
<222> (2221)..(2241)
<223> CK2

<220>
<221> misc_feature
<222> (2142)..(2235)
<223> Identical to the 5' CK cDNA

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tcacacctgg ttatatactat gatagttgta gacgattgcg taatgctatt aaatgcccat 180
cagtgtctggc tgtgacaccc aactgctgcc atttcgtgtt gacttgcacg agaaatgaga 240
aattgtctga ctatgcaggg tgtctatgcg tgggaacatt tatcagtggc cattaaatac 300
tatagtttac agtttagacca aagtgtgctg tatttttgtg ttagcttagc tgcagttttt 360
gtgtgtgaag taacaaatga caaatactca aactattgta attaatgagt ttttctcaga 420
aattgtaatt tactaagtag tttaaaaatg tgtactttta ctttcccttg agtacatttt 480
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cagccctccc catacataat cgtatgttta cacataggtt ggagttttaga gccataatct 1560
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aaagcctttc attaatgtga aagttgctgc gcgccccacc cagataaaaa gagcagaggt 1800


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actcaaagac acaggatccg g                                     2241

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<210> 8
<211> 1456
<212> DNA
<213> Danio rerio

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<220>
<221> TATA_signal
<222> (1389)..(1394)

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<220>
<221> primer_bind
<222> (1433)..(1456)
<223> MCK2

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<220>
<221> misc_feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA

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gcatgtgcac catgacagga ctgttattca cacttgggtg catgttggag actgttcggc 180
cagctatagt tttcttcaca gagtccctggg tcacctaatg tcacaaggaa gaaacatggt 240
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ttacagctta aaagattgct agacagaaaa accagggagg ggttttccca taatatccag 360
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acacaacagg gatagttcac ccaaaaaaaca gaccattctt tttttctgtt gaacaaaaat 540
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ggtgaacagg atccgg                                     1456

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<210> 9
 <211> 2205
 <212> DNA
 <213> Danio rerio
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 <221> primer_bind
 <222> (2179)..(2205)
 <223> ARP2

<220>
 <221> misc_feature
 <222> (2153)..(2199)
 <223> Identical to the 5' ARP cDNA

<220>
 <221> intron
 <222> (792)..(2152)

<220>
 <221> misc_feature
 <222> (775)..(791)
 <223> Identical to the 5' ARP cDNA

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 agaaataata caaatttggt tacagtattc ttagttattg caataaacga attttatata 180
 gaaagagaaa gagttttatt ataagatggt caatttaaaa aatggcagaa aatagaaaaa 240
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90 95 100

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35 40 45

Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
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Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
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15/pst/s

- 1 -

CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT TRANSGENIC ORNAMENTAL FISH

FIELD OF THE INVENTION

This invention relates to fish gene promoters and chimeric gene constructs with these
5 promoters for generation of transgenic fish, particularly fluorescent transgenic ornamental
fish.

BACKGROUND OF THE INVENTION

Transgenic technology involves the transfer of a foreign gene into a host organism
enabling the host to acquire a new and inheritable trait. The technique was first developed
10 in mice by Gordon et al. (1980). They injected foreign DNA into fertilized eggs and found
that some of the mice developed from the injected eggs retained the foreign DNA.
Applying the same technique, Palmiter et al. (1982) have introduced a chimeric gene
containing a rat growth hormone gene under a mouse heavy metal-inducible gene promoter
and generated the first batch of genetically engineered supermice, which are almost twice
15 as large as non-transgenic siblings. This work has opened a promising avenue in using the
transgenic approach to provide to animals new and beneficial traits for livestock husbandry
and aquaculture.

In addition to the stimulation of somatic growth for increasing the gross production
of animal husbandry and aquaculture, transgenic technology also has many other potential
20 applications. First of all, transgenic animals can be used as bioreactors to produce
commercially useful compounds by expression of a useful foreign gene in milk or in blood.
Many pharmaceutically useful protein factors have been expressed in this way. For
example, human α 1-antitrypsin, which is commonly used to treat emphysema, has been
expressed at a concentration as high as 35 mg/ml (10% of milk proteins) in the milk of
25 transgenic sheep (Wright et al., 1991). Similarly, the transgenic technique can also be used
to improve the nutritional value of milk by selectively increasing the levels of certain
valuable proteins such as caseins and by supplementing certain new and useful proteins
such as lysozyme for antimicrobial activity (Maga and Murray, 1995). Second, transgenic
mice have been widely used in medical research, particularly in the generation of
30 transgenic animal models for human disease studies (Lathe and Mullins, 1993). More
recently, it has been proposed to use transgenic pigs as organ donors for
xenotransplantation by expressing human regulators of complement activation to prevent
hyperacute rejection during organ transplantation (Cozzi and White, 1995). The

development of disease resistant animals has also been tested in transgenic mice (e.g. Chen et al., 1988).

Fish are also an intensive research subject of transgenic studies. There are many ways of introducing a foreign gene into fish, including: microinjection (e.g. Zhu et al., 1985; Du et al., 1992), electroporation (Powers et al., 1992), sperm-mediated gene transfer (Khoo et al., 1992; Sin et al., 1993), gene bombardment or gene gun (Zelegni et al., 1991), liposome-mediated gene transfer (Szelei et al., 1994), and the direct injection of DNA into muscle tissue (Xu et al., 1999). The first transgenic fish report was published by Zhu et al. (1985) using a chimeric gene construct consisting of a mouse metallothionein gene promoter and a human growth hormone gene. Most of the early transgenic fish studies have concentrated on growth hormone gene transfer with an aim of generating fast growing "superfish". A majority of early attempts used heterologous growth hormone genes and promoters and failed to produce gigantic superfish (e.g. Chourrout et al., 1986; Penman et al., 1990; Brem et al., 1988; Gross et al., 1992). But enhanced growth of transgenic fish has been demonstrated in several fish species including Atlantic salmon, several species of Pacific salmon, and loach (e.g. Du et al., 1992; Delvin et al., 1994, 1995; Tsai et al., 1995).

The zebrafish, *Danio rerio*, is a new model organism for vertebrate developmental biology. As an experimental model, the zebrafish offers several major advantages such as easy availability of eggs and embryos, tissue clarity throughout embryogenesis, external development, short generation time and easy maintenance of both the adult and the young. Transgenic zebrafish have been used as an experimental tool in zebrafish developmental biology. However, despite the fact that the first transgenic zebrafish was reported a decade ago (Stuart et al., 1988), most transgenic zebrafish work conducted so far used heterologous gene promoters or viral gene promoters: e.g. viral promoters from SV40 (simian virus 40) and RSV (Rous sarcoma virus) (Stuart et al., 1988, 1990; Bayer and Campos-Ortega, 1992), a carp actin promoter (Liu et al., 1990), and mouse homeobox gene promoters (Westerfield et al., 1992). As a result, the expression pattern of a transgene in many cases is variable and unpredictable.

GFP (green fluorescent protein) was isolated from a jelly fish, *Aequorea victoria*. The wild type GFP emits green fluorescence at a wavelength of 508 nm upon stimulation with ultraviolet light (395 nm). The primary structure of GFP has been elucidated by cloning of its cDNA and genomic DNA (Prasher et al., 1992). A modified GFP, also called EGFP (Enhanced Green Fluorescent Protein) has been generated artificially and it contains mutations that allow the protein to emit a stronger green light and its coding sequence has also been optimized for higher expression in mammalian cells based on preferable human

codons. As a result, EGFP fluorescence is about 40 times stronger than the wild type GFP in mammalian cells (Yang et al., 1996). GFP (including EGFP) has become a popular tool in cell biology and transgenic research. By fusing GFP with a tested protein, the GFP fusion-protein can be used as an indicator of the subcellular location of the tested protein (Wang and Hazelrigg, 1994). By transformation of cells with a functional GFP gene, the GFP can be used as a marker to identify expressing cells (Chalfie et al., 1994). Thus, the GFP gene has become an increasingly popular reporter gene for transgenic research as GFP can be easily detected by a non-invasive approach.

The GFP gene (including EGFP gene) has also been introduced into zebrafish in several previous reports by using various gene promoters, including *Xenopus elongation factor 1 α* enhancer-promoter (Amsterdam et al., 1995, 1996), rat *myosin light-chain* enhancer (Moss et al., 1996), zebrafish *GATA-1* and *GATA-3* promoters (Meng et al., 1997; Long et al., 1997), zebrafish α - and β -*actin* promoters (Higashijima et al., 1997), and tilapia *insulin-like growth factor I* promoter (Chen et al., 1998). All of these transgenic experiments aim at either developing a GFP transgenic system for gene expression analysis or at testing regulatory DNA elements in gene promoters.

SUMMARY OF THE INVENTION

It is a primary objective of the invention to clone fish gene promoters that are constitutive (ubiquitous), or that have tissue specificity such as skin specificity or muscle specificity or that are inducible by a chemical substance, and to use these promoters to develop effective gene constructs for production of transgenic fish.

It is another objective of the invention to develop fluorescent transgenic ornamental fish using these gene constructs. By applying different gene promoters, tissue-specific, inducible under different environmental conditions, or ubiquitous, to drive the GFP gene, GFP could be expressed in different tissues or ubiquitously. Thus, these transgenic fish may be skin fluorescent, muscle fluorescent, ubiquitously fluorescent, or inducibly fluorescent. These transgenic fish may be used for ornamental purposes, for monitoring environmental pollution, and for basic studies such as recapitulation of gene expression programs or monitoring cell lineage and cell migration. These transgenic fish may be used for cell transplantation and nuclear transplantation or fish cloning.

Other objectives, features and advantages of the present invention will become apparent from the detailed description which follows, or may be learned by practice of the invention.

Four zebrafish gene promoters of different characteristics were isolated and four chimeric gene constructs containing a zebrafish gene promoter and EGFP DNA were made: pCK-EGFP, pMCK-EGFP, pMLC2f-EGFP and pARP-EGFP. The first chimeric gene-construct, pCK-EGFP, contains a 2.2 kbp polynucleotide comprising a zebrafish
5 cytotkeratin (CK) gene promoter which is specifically or predominantly expressed in skin epithelia. The second one, pMCK-EGFP, contains a 1.5 kbp polynucleotide comprising a muscle-specific promoter from a zebrafish muscle creatine kinase (MCK) gene and the gene is only expressed in the muscle tissue. The third construct, pMLC2f-EGFP contains a
10 2.2 kbp polynucleotide comprising a strong skeletal muscle-specific promoter from the fast skeletal muscle isoform of the myosin light chain 2 (MLC2f) gene and is expressed specifically or predominantly in skeletal muscle. The fourth chimeric gene construct, pARP-EGFP, contains a strong and ubiquitously expressed promoter from a zebrafish
acidic ribosomal protein (ARP) gene. These four chimeric gene constructs have been introduced into zebrafish at the one cell stage or two cell stage by microinjection. In all
15 cases, the GFP expression patterns were consistent with the specificities of the promoters. GFP was predominantly expressed in skin epithelia with pCK-EGFP, specifically expressed in muscles with pMCK-EGFP, specifically expressed in skeletal muscles with pMLC2f-EGFP and ubiquitously expressed in all tissues with pARP-EGFP.

These chimeric gene constructs are useful to generate green fluorescent transgenic
20 fish. The GFP transgenic fish emit green fluorescence light under a blue or ultraviolet light and this feature makes the genetically engineered fish unique and attractive in the ornamental fish market. The fluorescent transgenic fish are also useful for the development of a biosensor system and as research models for embryonic studies such as cell lineage, cell migration, cell and nuclear transplantation etc.

25 BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1A-II are photographs showing expression of CK (Figs. 1A-1C), MCK (Figs. 1D-1E), ARP (Figs. 1F-1G) and MLC2f (Figs. 1H-1I) mRNAs in zebrafish embryos as revealed by whole mount *in situ* hybridization (detailed description of the procedure can be found in Thisse et al., 1993). (Fig. 1A) A 28 hpf (hour postfertilization) embryo hybridized
30 with a CK antisense riboprobe. (Fig. 1B) Enlargement of the mid-part of the embryo shown in Fig. 1A. (Fig. 1C) Cross-section of the embryo in Fig. 1A. (Fig. 1D) A 30 hpf embryo hybridized with an MCK antisense riboprobe. (Fig. 1E) Cross-section of the embryo in Fig 1D. (Fig. 1F) A 28 hpf embryo hybridized with an ARP antisense riboprobe. (Fig. 1G) Cross-section of the embryo in Fig. 1F. Arrows indicate the planes for cross-
35 sections and the box in panel A indicates the enlarged region shown in panel B. (Fig. 1H) Side view of a 22-hpf embryo hybridized with the MLC2f probe. (Fig. 1I) Transverse

section through the trunk of a stained 24-hpf embryo. SC, spinal cord; N, notochord.

Fig. 2A is a digitized image showing distribution of CK, MCK and ARP mRNAs in adult tissues. Total RNAs were prepared from selected adult tissues as indicated at the top of each lane and analyzed by Northern blot hybridization (detailed description of the procedure can be found in Gong et al., 1992). Three identical blots were made from the same set of RNAs and hybridized with the CK, MCK and ARP probes, respectively.

Fig. 2B is a digitized image showing distribution of MLC2f mRNA in adult tissues. Total RNAs were prepared from selected adult tissues as indicated at the top of each lane and analyzed by Northern blot hybridization (detailed description of the procedure can be found in Gong et al., 1992). Two identical blots were made from the same set of RNAs and hybridized with the MLC2f probe and a ubiquitously expressed α -actin probe, respectively.

Fig. 3. is a schematic representation of the strategy of promoter cloning. Restriction enzyme digested genomic DNA was ligated with a short linker DNA which consists of Oligo 1 and Oligo 2. Nested PCR reactions were then performed: the first round PCR used linker specific primer L1 and gene specific primers G1, where G1 is CK1, MCK1, M1 or ARP1 in the described embodiments, and the second round linker specific primer L2 and gene specific primer G2, where G2 is CK2, MCK2, M2 or ARP2, respectively in the described embodiments.

Fig. 4 is a schematic map of the chimeric gene construct, pCK-EGFP. The 2.2 kb zebrafish DNA fragment comprising the CK promoter region is inserted into pEGFP-1 (Clontech) at the EcoRI and BamHI site as indicated. In the resulting chimeric DNA construct, the EGFP gene is under control of the zebrafish CK promoter. Also shown is the kanamycin/neomycin resistance gene (Kan^r/Neo^r) in the backbone of the original pEGFP-1 plasmid. The total length of the recombinant plasmid pCK-EGFP is 6.4 kb.

Fig. 5 is a schematic map of the chimeric gene construct, pMCK-EGFP. The 1.5 kb zebrafish DNA fragment comprising the MCK promoter region is inserted into pEGFP-1 (Clontech) at the EcoRI and BamHI site as indicated. In the resulting chimeric DNA construct, the EGFP gene is under control of the zebrafish MCK promoter. Also shown is the kanamycin/neomycin resistance gene (Kan^r/Neo^r) in the backbone of the original pEGFP-1 plasmid. The total length of the recombinant plasmid pMCK-EGFP is 5.7 kb.

Fig. 6 is a schematic map of the chimeric gene construct, pARP-EGFP. The 2.2 kb zebrafish DNA fragment comprising the ARP promoter/1st intron region is inserted into pEGFP-1 (Clontech) at the EcoRI and BamHI site as indicated. In the resulting chimeric

DNA construct, the EGFP gene is under control of the zebrafish ARP promoter. Also shown is the kanamycin/neomycin resistance gene (Kan^r/Neo^r) in the backbone of the original pEGFP-1 plasmid. The total length of the recombinant plasmid pARP-EGFP is 6.4 kb. —

- 5 Fig. 7 is a schematic map of the chimeric gene construct, pMLC2f-EGFP. The 2.0 kb zebrafish DNA fragment comprising the MLC2f promoter region is inserted into pEGFP-1 (Clontech) at the HindIII and BamHI site as indicated. In the resulting chimeric DNA construct, the EGFP gene is under control of the zebrafish MLC2f promoter. Also shown is the kanamycin/neomycin resistance gene (Kan^r/Neo^r) in the backbone of the original pEGFP-1 plasmid. The total length of the recombinant plasmid pMLC2f-EGFP is 6.2 kb.

Fig. 8 is a photograph of a typical transgenic zebrafish fry (4 days old) with pCK-EGFP, which emits green fluorescence from skin epithelia under a blue light.

- 15 Fig. 9 is a photograph of a typical transgenic zebrafish fry (3 days old) with pMCK-EGFP, which emits green fluorescence from skeletal muscles under a blue light.

Fig. 10 is a photograph of a typical transgenic zebrafish fry (2 days old) with pARP-EGFP, which emits green fluorescence under a blue light from a variety of cell types such as skin epithelia, muscle cells, lens, neural tissues, notochord, circulating blood cells and yolk cells.

Figs. 11A-11B. Photographs of a typical transgenic zebrafish founder with pMLC2f-EGFP (Fig. 11A) and an F1 stable transgenic offspring (Fig. 11B). Both pictures were taken under an ultraviolet light (365 nm). The green fluorescence can be better observed under a blue light with an optimal wavelength of 488 nm.

Figs. 12A-12C. Examples of high, moderate and low expression of GFP in transiently transgenic embryos at 72 hpf. (Fig. 12A) High expression, GFP expression was detected in essentially 100% of the muscle fibers in the trunk. (Fig. 12B) Moderate expression, GFP expression was detected in several bundles of muscle fibers, usually in the mid-trunk region. (Fig. 12C) Low expression, GFP expression occurred in dispersed muscle fibers and the number of GFP positive fibers is usually less than 20 per embryo.

Fig. 13. Deletion analysis of the MLC2f promoter in transient transgenic zebrafish embryos. A series of 5' deletions of MLC2f-EGFP constructs containing -2011-bp (2-kb), -1338-bp, -873-bp, -283-bp, -77-bp and -3-bp of the MLC2f promoter were generated by unidirectional deletion using the double-stranded Nested Deletion Kit from Pharmacia

based on the manufacturer's instructional manual. Each construct was injected into approximately 100 embryos and GFP expression was monitored in the first 72 hours of embryonic development. The level of GFP expression was classified based on the examples shown in Figs. 12A-12C. Potential E-boxes and MEF2 binding sites, which are important for muscle-specific transcription (Schwarz et al., 1993; Olson et al., 1995), are indicated on the -2011-bp construct.

DETAILED DESCRIPTION OF THE INVENTION

Gene Constructs

To develop successful transgenic fish with a predictable pattern of transgene expression, the first step is to make a gene construct suitable for transgenic studies. The gene construct generally comprises three portions: a gene promoter, a structural gene and transcriptional termination signals. The gene promoter would determine where, when and under what conditions the structural gene is turned on. The structural gene contains protein coding portions that determine the protein to be synthesized and thus the biological function. The structural gene might also contain intron sequences which can affect mRNA stability or which might contain transcription regulatory elements. The transcription termination signals consist of two parts: a polyadenylation signal and a transcriptional termination signal after the polyadenylation signal. Both are important to terminate the transcription of the gene. Among the three portions, selection of a promoter is very important for successful transgenic study, and it is preferable to use a homologous promoter (homologous to the host fish) to ensure accurate gene activation in the transgenic host.

A promoter drives expression "predominantly" in a tissue if expression is at least 2-fold, preferably at least 5-fold higher in that tissue compared to a reference tissue. A promoter drives expression "specifically" in a tissue if the level of expression is at least 5-fold, preferably at least 10-fold higher, more preferably at least 50-fold higher in that tissue than in any other tissue.

Recombinant DNA Constructs

Recombinant DNA constructs comprising one or more of the DNA or RNA sequences described herein and an additional DNA and/or RNA sequence are also included within the scope of this invention. These recombinant DNA constructs usually have sequences which do not occur in nature or exist in a form that does not occur in nature or exist in association with other materials that do not occur in nature. The DNA and/or RNA sequences described as constructs or in vectors above are "operably linked" with other

DNA and/or RNA sequences. DNA regions are operably linked when they are functionally related to each other. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as part of a preprotein which participates in the secretion of the polypeptide; a promoter is operably linked to a coding sequence if it controls the transcription of the coding sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit translation. Generally, operably linked means contiguous (or in close proximity to) and, in the case of secretory leaders, contiguous and in reading phase.

The sequences of some of the DNAs, and the corresponding proteins encoded by the DNA, which are useful in the invention are set forth in the attached Sequence Listing.

The complete cytokeratin (CK) cDNA sequence is shown in SEQ ID NO:1, and its deduced amino acid sequence is shown in SEQ ID NO:2. The binding sites of the gene specific primers for promoter amplification, CK1 and CK2, are indicated. The extra nucleotides introduced into CK2 for generation of a restriction site are shown as a misc_feature in the primer sequence SEQ ID NO:11. A potential polyadenylation signal, AATAAA, is indicated in SEQ ID NO:1.

The complete muscle creatine kinase (MCK) cDNA sequence is shown in SEQ ID NO:3, and its deduced amino acid sequence is shown in SEQ ID NO:4. The binding sites of the gene specific primers for promoter amplification, MCK1 and MCK2, are indicated. The extra nucleotides introduced into MCK1 and MCK2 for generation of restriction sites are shown as a misc_feature in the primer sequences SEQ ID NOS:12 and 13, respectively. A potential polyadenylation signal, AATAAA, is indicated in SEQ ID NO:3.

The complete fast skeletal muscle isoform of myosin light chain 2 (MLC2f) cDNA sequence is shown in SEQ ID NO:20, and its deduced amino acid sequence is shown in SEQ ID NO:21. The binding sites of the gene-specific primers for promoter amplification, M1 and M2, are indicated. Two potential polyadenylation signals, AATAAA, are shown as a misc_feature in SEQ ID NO:20.

The complete acidic ribosomal protein P0 (ARP) cDNA sequence is shown in SEQ ID NO:5, and its deduced amino acid sequence is shown in SEQ ID NO:6. The binding sites of the gene specific primers for promoter amplification, ARP1 and ARP2, are indicated. The extra nucleotides introduced into ARP2 for generation of a restriction site are shown as a misc_feature in the primer sequence SEQ ID NO:15. A potential polyadenylation signal, AATAAA, is indicated in SEQ ID NO:5.

SEQ ID NO:7 shows the complete sequence of the CK promoter region. A putative

TATA box is shown, and the 3' nucleotides identical to the 5' CK cDNA sequence are shown as a misc_feature. The binding site of the second gene specific primer, CK2, is shown. The introduced BamHI site is indicated as a misc_feature in the primer sequence SEQ ID NO:11.

5 SEQ ID NO:8 shows the complete sequence of the MCK promoter region. A putative TATA box is shown, and the 3' nucleotides identical to the 5' MCK cDNA sequence are shown as a misc_feature in SEQ ID NO:8. The binding site of the second gene specific primer, MCK2, is shown. The introduced BamHI site is indicated as a misc_feature in the primer sequence SEQ ID NO:13.

10 SEQ ID NO:22 shows the complete sequence of the MLC2f promoter region. A putative TATA box is shown, and the 3' nucleotides identical to the 5' MLC2f cDNA sequence are shown as a misc_feature. The binding site of the second gene-specific primer, M2, is shown. Potential muscle-specific cis-elements, E-boxes and MEF2 binding sites, are also shown. The proximal 1-kb region of the MLC2f promoter was recently published (Xu
15 et al., 1999).

SEQ ID NO:9 shows the complete sequence of the ARP promoter region including the first intron. The first intron is shown, and the 3' nucleotides identical to the 5' ARP cDNA sequence are shown as misc_features. No typical TATA box is found. The binding site of the second gene specific primer, ARP2, is shown. The introduced BamHI site is
20 indicated as a misc_feature in the primer sequence SEQ ID NO:15.

Specifically Exemplified Polypeptides/DNA

The present invention contemplates use of DNA that codes for various polypeptides and other types of DNA to prepare the gene constructs of the present invention. DNA that codes for structural proteins, such as fluorescent peptides including GFP, EGFP, BFP, EBFP, YFP, EYFP, CFP, ECFP and enzymes (such as luciferase, β -galactosidase, chloramphenicol acetyltransferase, etc.), and hormones (such as growth hormone etc.), are
25 useful in the present invention. More particularly, the DNA may code for polypeptides comprising the sequences exemplified in SEQ ID NOS:2, 4, 6 and 21. The present invention also contemplates use of particular DNA sequences, including regulatory
30 sequences, such as promoter sequences shown in SEQ ID NOS: 7, 8, 9 and 22 or portions thereof effective as promoters. Finally, the present invention also contemplates the use of additional DNA sequences, described generally herein or described in the references cited herein, for various purposes.

Chimeric Genes

The present invention also encompasses chimeric genes comprising a promoter described herein operatively linked to a heterologous gene. Thus, a chimeric gene can comprise a promoter of a zebrafish operatively linked to a zebrafish structural gene other than that normally found linked to the promoter in the genome. Alternatively, the promoter can be operatively linked to a gene that is exogenous to a zebrafish, as exemplified by the GFP and other genes specifically exemplified herein. Furthermore, a chimeric gene can comprise an exogenous promoter linked to any structural gene not normally linked to that promoter in the genome of an organism.

10 Variants of Specifically Exemplified Polypeptide

DNA that codes for variants of the specifically exemplified polypeptides are also encompassed by the present invention. Possible variants include allelic variants and corresponding polypeptides from other organisms, particularly other organisms of the same species, genus or family. The variants may have substantially the same characteristics as the natural polypeptides. The variant polypeptide will possess the primary property of concern for the polypeptide. For example, the polypeptide will possess one or more or all of the primary physical (e.g., solubility) and/or biological (e.g., enzymatic activity, physiologic activity or fluorescence excitation or emission spectrum) properties of the reference polypeptide. DNA of the structural genes of the present invention will encode a protein that produces a fluorescent or chemiluminescent light under conditions appropriate to the particular polypeptide in one or more tissues of a fish. Preferred tissues for expression are skin, muscle, eye and bone.

Substitutions, Additions and Deletions

As possible variants of the above specifically exemplified polypeptides, the polypeptide may have additional individual amino acids or amino acid sequences inserted into the polypeptide in the middle thereof and/or at the N-terminal and/or C-terminal ends thereof so long as the polypeptide possesses the desired physical and/or biological characteristics. Likewise, some of the amino acids or amino acid sequences may be deleted from the polypeptide so long as the polypeptide possesses the desired physical and/or biochemical characteristics. Amino acid substitutions may also be made in the sequences so long as the polypeptide possesses the desired physical and biochemical characteristics. DNA coding for these variants can be used to prepare gene constructs of the present invention.

Sequence Identity

The variants of polypeptides or polynucleotides contemplated herein should possess more than 75% sequence identity (sometimes referred to as homology), preferably more than 85% identity, most preferably more than 95% identity, even more preferably
5 more than 98% identity to the naturally occurring and/or specifically exemplified sequences or fragments thereof described herein. To determine this homology, two sequences are aligned so as to obtain a maximum match using gaps and inserts.

Two sequences are said to be "identical" if the sequence of residues is the same when aligned for maximum correspondence as described below. The term
10 "complementary" applies to nucleic acid sequences and is used herein to mean that the sequence is complementary to all or a portion of a reference polynucleotide sequence.

Optimal alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment method of Needleman and Wunsch (1970), by the search for similarity method of Pearson and
15 Lippman (1988), or the like. Computer implementations of the above algorithms are known as part of the Genetics Computer Group (GCG) Wisconsin Genetics Software Package (GAP, BESTFIT, BLASTA, FASTA and TFASTA), 575 Science Drive, Madison, WI. These programs are preferably run using default values for all parameters.

"Percentage of sequence identity" is determined by comparing two optimally
20 aligned sequences over a comparison window, wherein the portion of the sequence in the comparison window may comprise additions or deletions (*i.e.* "gaps") as compared to the reference sequence for optimal alignment of the two sequences being compared. The percentage identity is calculated by determining the number of positions at which the identical residue occurs in both sequences to yield the number of matched positions,
25 dividing the number of matched positions by the total number of positions in the window and multiplying the result by 100 to yield the percentage of sequence identity. Total identity is then determined as the average identity over all of the windows that cover the complete query sequence.

Fragments of Polypeptide

30 Genes which code for fragments of the full length polypeptides such as proteolytic cleavage fragments which contain at least one, and preferably all, of the above-listed physical and/or biological properties are also encompassed by the present invention.

DNA and RNA

The invention encompasses DNA that codes for any one of the above-described polypeptides including, but not limited to, those shown in SEQ ID NOS:2, 4, 6 and 21 including fusion polypeptides, variants and fragments thereof. The sequence of certain particularly useful cDNAs which encode polypeptides are shown in SEQ ID NOS:1, 3, 5 and 20. The present invention also includes cDNA as well as genomic DNA containing or comprising the requisite nucleotide sequences as well as corresponding RNA and antisense sequences.

Cloned DNA within the scope of the invention also includes allelic variants of the specific sequences presented in the attached Sequence Listing. An "allelic variant" is a sequence that is a variant from that of the exemplified nucleotide sequence, but represents the same chromosomal locus in the organism. In addition to those which occur by normal genetic variation in a population and perhaps fixed in the population by standard breeding methods, allelic variants can be produced by genetic engineering methods. A preferred allelic variant is one that is found in a naturally occurring organism, including a laboratory strain. Allelic variants are either silent or expressed. A silent allele is one that does not affect the phenotype of the organism. An expressed allele results in a detectable change in the phenotype of the trait represented by the locus.

A nucleic acid sequence "encodes" or "codes for" a polypeptide if it directs the expression of the polypeptide referred to. The nucleic acid can be DNA or RNA. Unless otherwise specified, a nucleic acid sequence that encodes a polypeptide includes the transcribed strand, the hnRNA and the spliced RNA or the DNA representative of the mRNA. An "antisense" nucleic acid is one that is complementary to all or part of a strand representative of mRNA, including untranslated portions thereof.

Degenerate Sequences

In accordance with degeneracy of genetic code, it is possible to substitute at least one base of the base sequence of a gene by another kind of base without causing the amino acid sequence of the polypeptide produced from the gene to be changed. Hence, the DNA of the present invention may also have any base sequence that has been changed by substitution in accordance with degeneracy of genetic code.

DNA Modification

The DNA is readily modified by substitution, deletion or insertion of nucleotides, thereby resulting in novel DNA sequences encoding the polypeptide or its derivatives.

These modified sequences are used to produce mutant polypeptide and to directly express the polypeptide. Methods for saturating a particular DNA sequence with random mutations and also for making specific site-directed mutations are known in the art; see *e.g.* Sambrook et al. (1989).

5 Hybridizable Variants

The DNA molecules useful in accordance with the present invention can comprise a nucleotide sequence selected from the group consisting of SEQ ID NOS.:1, 3, 5, 7-20 and 22-24 or can comprise a nucleotide sequence that hybridizes to a DNA molecule comprising the nucleotide sequence of SEQ ID NOS.:1, 3, 5 or 20 under salt and temperature conditions providing stringency at least as high as that equivalent to 5x SSC and 42°C and that codes on expression for a polypeptide that has one or more or all of the above-described physical and/or biological properties. The present invention also includes polypeptides coded for by these hybridizable variants. The relationship of stringency to hybridization and wash conditions and other considerations of hybridization can be found in Chapters 11 and 12 of Sambrook et al (1989). The present invention also encompasses functional promoters which hybridize to SEQ ID NOS:7, 8, 9 or 22 under the above-described conditions. DNA molecules of the invention will preferably hybridize to reference sequences under more stringent conditions allowing the degree of mismatch represented by the degrees of sequence identity enumerated above. The present invention also encompasses functional primers or linker oligonucleotides set forth in SEQ ID NOS:10-19 and 23-24 or larger primers comprising these sequences, or sequences which hybridize with these sequences under the above-described conditions. The primers usually have a length of 10-50 nucleotides, preferably 15-35 nucleotides, more preferably 18-30 nucleotides.

25 Vectors

The invention is further directed to a replicable vector containing cDNA that codes for the polypeptide and that is capable of expressing the polypeptide.

The present invention is also directed to a vector comprising a replicable vector and a DNA sequence corresponding to the above described gene inserted into said vector. The vector may be an integrating or non-integrating vector depending on its intended use and is conveniently a plasmid.

Transformed Cells

The invention further relates to a transformed cell or microorganism containing cDNA or a vector which codes for the polypeptide or a fragment or variant thereof and that

is capable of expressing the polypeptide.

Expression Systems Using Vertebrate Cells

Interest has been great in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of vertebrate host cell lines useful in the present invention preferably include cells from any of the fish described herein. Expression vectors for such cells ordinarily include (if necessary) an origin of replication, a promoter located upstream from the gene to be expressed, along with a ribosome-binding site, RNA splice site (if intron-containing genomic DNA is used or if an intron is necessary to optimize expression of a cDNA), a polyadenylation site, and a transcription termination sequence.

EXAMPLES

The following examples are provided by way of illustration only and not by way of limitation. Those of skill will readily recognize a variety of noncritical parameters which can be changed or modified to yield essentially similar results.

15 **Example I: Isolation of skin-specific, muscle-specific and ubiquitously expressed zebrafish cDNA clones.**

cDNA clones were isolated and sequenced as described by Gong et al. (1997). Basically, random cDNA clones were selected from zebrafish embryonic and adult cDNA libraries and each clone was partially sequenced by a single sequencing reaction. The partial sequences were then used to identify the sequenced clones for potential function and tissue specificity. Of the distinct clones identified by this approach, four of them were selected: for skin specificity (clone A39 encoding cytokeratin, CK), for muscle specificity (clone E146 encoding muscle creatine kinase, MCK), for skeletal muscle specificity (clone A113 encoding the fast skeletal muscle isoform of the myosin light chain 2, MLC2f) and for ubiquitous expression (clone A150 encoding acidic ribosomal protein P0, ARP), respectively.

The four cDNA clones were sequenced, and their complete cDNA sequences with deduced amino acid sequences are shown in SEQ ID NOS:1, 3, 5, and 20 respectively. A39 encodes a type II basic cytokeratin and its closest homolog in mammals is cytokeratin 8 (65-68% amino acid identity). E146 codes for the zebrafish MCK and its amino acid sequence shares ~87% identity with mammalian MCKs. A113 encodes the fast skeletal muscle isoform of the myosin light chain 2. The deduced amino acid sequence of this gene is highly homologous to other vertebrate fast skeletal muscle MLC2f proteins (over 80%

amino acid identity). The amino acid sequence of zebrafish ARP deduced from the A150 clone is 87-89% identical to those of mammalian ARPs.

To demonstrate their expression patterns, whole mount *in situ* hybridization (Thisse et al., 1993) was performed for developing embryos and Northern blot analyses (Gong et al., 1992) were carried out for selected adult tissues and for developing embryos.

As indicated by whole mount *in situ* hybridization, cytokeratin mRNA was specifically expressed in the embryonic surface (Figs. 1A-1C) and cross section of *in situ* hybridized embryos confirmed that the expression was only in skin epithelia (Fig. 1C). Ontogenetically, the cytokeratin mRNA appeared before 4 hours post-fertilization (hpf) and it is likely that the transcription of the cytokeratin gene starts at mid-blastula transition when the zygotic genome is activated. By *in situ* hybridization, a clear cytokeratin mRNA signal was detected in highly flattened cells of the superficial layer in blastula and the expression remained in the superficial layer which eventually developed into skin epithelia including the yolk sac. In adult tissues, cytokeratin mRNA was predominantly detected in the skin and also weakly in several other tissues including the eye, gill, intestine and muscle, but not in the liver and ovary (Fig. 2). Therefore, the cytokeratin mRNA is predominantly, if not specifically, expressed in skin cells.

MCK mRNA was first detected in the first few anterior somites in 10 somite stage embryos (14 hpf) and at later stages the expression is specifically in skeletal muscle (Fig. 1D) and in heart (data not shown). When the stained embryos are cross-sectioned, the MCK mRNA signal was found exclusively in the trunk skeletal muscles (Fig. 1E). In adult tissues, MCK mRNA was detected exclusively in the skeletal muscle (Fig. 2).

MLC2f mRNA was specifically expressed in fast skeletal muscle in developing zebrafish embryos (Figs. 1H-1I). To examine the tissue distribution of MLC2f mRNA, total RNAs were prepared from several adult tissues including heart, brain, eyes, gills, intestine, liver, skeletal muscle, ovary, skin, and testis. MLC2f mRNA was only detected in the skeletal muscle by Northern analysis; while α -actin mRNA was detected ubiquitously in the same set of RNAs, confirming the validity of the assay (Fig. 2B).

ARP mRNA was expressed ubiquitously and it is presumably a maternal mRNA since it is present in the ovary as well as in embryos at one cell stage. In *in situ* hybridization experiments, an intense hybridization signal was detected in most tissues. An example of a hybridized embryo at 28 hpf is shown in Fig. 1F. In adults, ARP mRNA was abundantly expressed in all tissues examined except for the brain where a relatively weak signal was detected (Fig. 2A). These observations confirmed that the ARP mRNA is expressed ubiquitously.

Example II: Isolation of zebrafish gene promoters

Four zebrafish gene promoters were isolated by a linker-mediated PCR method as described by Liao *et al.*, (1997) and as exemplified by the diagrams in Fig. 3. The whole procedure includes the following steps: 1) designing of gene specific primers; 2) isolation of zebrafish genomic DNA; 3) digestion of genomic DNA by a restriction enzyme; 4) ligation of a short linker DNA to the digested genomic DNA; 5) PCR amplification of the promoter region; and 6) DNA sequencing to confirm the cloned DNA fragment. The following is the detailed description of these steps.

1. Designing of gene specific primers

- 10 Gene specific PCR primers were designed based on the 5' end of the four cDNA sequences and the regions used for designing the primers are shown in SEQ ID NOS: 1, 3, 5 and 20.

The two cytokeratin gene specific primers are:

CK1 (SEQ ID NO:10)

- 15 CK2 (SEQ ID NO:11), where the first six nucleotides are for creation of an EcoRI site to facilitate cloning.

The two muscle creatine kinase gene specific primers are:

MCK1 (SEQ ID NO:12), where the first five nucleotides are for creation of an EcoRI site to facilitate cloning.

- 20 MCK2 (SEQ ID NO:13), where the first three nucleotides are for creation of an EcoRI site to facilitate cloning.

The two fast skeletal muscle isoform of myosin light chain 2 gene specific primers are:

M1 (SEQ ID NO:23)

M2 (SEQ ID NO:24)

- 25 The two acidic ribosomal protein P0 gene specific primers are:

ARP1 (SEQ ID NO:14)

ARP2 (SEQ ID NO:15), where the first six nucleotides are for creation of an EcoRI site to facilitate cloning.

2. Isolation of zebrafish genomic DNA

Genomic DNA was isolated from a single individual fish by a standard method (Sambrook
5 *et al.*, 1989). Generally, an adult fish was quickly frozen in liquid nitrogen and ground into powder. The ground tissue was then transferred to an extraction buffer (10 mM Tris, pH 8, 0.1 M EDTA, 20 µg/ml RNase A and 0.5% SDS) and incubated at 37°C for 1 hour. Proteinase K was added to a final concentration of 100 µg/ml and gently mixed until the mixture appeared viscous, followed by incubation at 50°C for 3 hours with periodical
10 swirling. The genomic DNA was gently extracted three times by phenol equilibrated with Tris-HCl (pH 8), precipitated by adding 0.1 volume of 3 M NaOAc and 2.5 volumes of ethanol, and collected by swirling on a glass rod, then rinsed in 70% ethanol.

3. Digestion of genomic DNA by a restriction enzyme

Genomic DNA was digested with the selected restriction enzymes. Generally, 500
15 units of restriction enzyme were used to digest 50 µg of genomic DNA overnight at the optimal enzyme reaction temperature (usually at 37°C).

4. Ligation of a short linker DNA to the digested genomic DNA

The linker DNA was assembled by annealing equal moles of the two linker oligonucleotides, Oligo1 (SEQ ID NO:16) and Oligo 2 (SEQ ID NO:17). Oligo 2 was
20 phosphorylated by T4 polynucleotide kinase prior to annealing. Restriction enzyme digested genomic DNA was filled-in or trimmed with T4 DNA polymerase, if necessary, and ligated with the linker DNA. Ligation was performed with 1 µg of digested genomic DNA and 0.5 µg of linker DNA in a 20 µl reaction containing 10 units of T4 DNA ligase at 4°C overnight.

25 5. PCR amplification of promoter region

PCR was performed with Advantage Tth Polymerase Mix (Clontech). The first round of PCR was performed using a linker specific primer L1 (SEQ ID NO:18) and a gene specific primer G1 (CK1, MCK1, M1 or ARP1). Each reaction (50 µl) contains 5 µl of 10x Tth PCR reaction buffer (1X= 15 mM KOAc, 40 mM Tris, pH 9.3), 2.2 µl of 25
30 mM Mg(OAc)₂, 5 µl of 2 mM dNTP, 1 µl of L1 (0.2 µg/µl), 1 µl of G1 (0.2 µg/µl), 33.8

μl of H₂O, and 1 μl (50 ng) of linker ligated genomic DNA and 1 μl of 50x Tth polymerase mix (Clontech). The cycling conditions were as follows: 94°C/1 min, 35 cycles of 94°C/30 sec and 68°C/6 min, and finally 68°C/8 min. After the primary round of PCR was completed, the products were diluted 100 fold. One μl of diluted PCR product was used as template for the second round of PCR (nested PCR) with a second linker specific primer L2 (SEQ ID NO:19) and a second gene specific primer G2 (CK2, MCK2, M2 or ARP2), as described for the primary PCR but with the following modification: 94°C/1 min, 25 cycles of 94°C/30 sec and 68°C/6 min, and finally 68°C/8 min. Both the primary and secondary PCR products were analyzed on a 1% agarose gel.

10 6. DNA sequencing to confirm the cloned DNA fragment

PCR products were purified from the agarose gel following electrophoresis and cloned into a TA vector, pT7Blue™ (Novogen). DNA sequencing was performed by dideoxynucleotide chain termination method using a T7 Sequencing Kit purchased from Pharmacia. Complete sequences of these promoter regions were obtained by automatic sequencing using a dRhodamine Terminator Cycle Sequencing Ready Reaction Kit (Perkin-Elmer) and an ABI 377 automatic sequencing machine.

The isolated cytokeratin DNA fragment comprising the gene promoter is 2.2 kb. In the 3' proximal region immediately upstream of a portion identical to the 3' part of the CK cDNA sequence, there is a putative TATA box perfectly matching to a consensus TATA box sequence. The 164 bp of the 3' region is identical to the 5' UTR (untranslated region) of the cytokeratin cDNA. Thus, the isolated fragment was indeed derived from the same gene as the cytokeratin cDNA clone (SEQ ID NO:7). Similarly, a 1.5 kb 5' flanking region was isolated from the muscle creatine kinase gene, a putative TATA box was also found in its 3' proximal region and the 3' region is identical to the 5' portion of the MCK cDNA clone (SEQ ID NO:8). For MLC2f, a 2 kb region was isolated from the fast skeletal muscle isoform of myosin light chain 2 gene and sequenced completely. The promoter sequence for MLC2f is shown in SEQ ID NO:22. The sequence immediately upstream of the gene specific primer M2 is identical to the 5' UTR of the MLC2f cDNA clone; thus, the amplified DNA fragments are indeed derived from the MLC2f gene. A perfect TATA box was found 30 nucleotides upstream of the transcription start site, which was defined by a primer extension experiment based on Sambrook et al. (1989). In the 2-kb region comprising the promoter, six E-boxes (CANNTG) and six potential MEF2 binding sites [C(T)TA(T/A)4TA(A/G)] were found and are indicated in SEQ ID NO:22. Both of these cis-element classes are important for muscle specific gene transcription (Schwarz *et al.*, 1993; Olson *et al.*, 1995). A 2.2 kb fragment was amplified for the ARP gene. By

alignment of its sequence with the ARP cDNA clone, a 1.3 kb intron was found in the 5' UTR (SEQ ID NO:9). As a result, the isolated ARP promoter is within a DNA fragment about 0.8 kb long.

Example III: Generation of green fluorescent transgenic fish

5 The isolated zebrafish gene promoters were inserted into the plasmid pEGFP-1 (Clontech), which contains an EGFP structural gene whose codons have been optimized according to preferable human codons. Three promoter fragments were inserted into pEGFP-1 at the EcoRI and BamHI site and the resulting recombinant plasmids were named pCK-EGFP (Fig. 4), pMCK-EGFP (Fig. 5), and pARP-EGFP, respectively (Fig. 6). The
10 promoter fragment for the MLC2f gene was inserted into the Hind III and Bam HI sites of the plasmid pEGFP-1 and the resulting chimeric DNA construct, pMLC2f-EGFP, is diagramed in Fig. 7.

Linearized plasmid DNAs at a concentrations of 500 µg/ml (for pCK-EGFP and pMCK-EGFP) and 100 µg/ml (for pMLC2f-EGFP) in 0.1 M Tris-HCl (pH 7.6)/0.25%
15 phenol red were injected into the cytoplasm of 1- or 2-cell stage embryos. Because of a high mortality rate, pARP-EGFP was injected at a lower concentration (50 µg/ml). Each embryo received 300-500 pl of DNA. The injected embryos were reared in autoclaved Holtfreter's solution (0.35% NaCl, 0.01% KCl and 0.01% CaCl₂) supplemented with 1 µg/ml of methylene blue. Expression of GFP was observed and photographed under a
20 ZEISS Axiovert 25 fluorescence microscope.

When zebrafish embryos received pCK-EGFP, GFP expression started about 4 hours after injection, which corresponds to the stage of ~30% epiboly. About 55% of the injected embryos expressed GFP at this stage. The early expression was always in the superficial layer of cells, mimicking endogenous expression of the CK gene as observed by
25 *in situ* hybridization. At later stages, in all GFP-expressing fish, GFP was found predominantly in skin epithelia. A typical pCK-EGFP transgenic zebrafish fry at 4 days old is shown in Fig. 8.

Under the MCK promoter, no GFP expression was observed in early embryos before muscle cells become differentiated. By 24 hpf, about 12% of surviving embryos
30 expressed GFP strongly in muscle cells and these GFP-positive embryos remain GFP-positive after hatching. The GFP expression was always found in many bundles of muscle fibers, mainly in the mid-trunk region and no expression was ever found in other types of cells. A typical pMCK-EGFP transgenic zebrafish fry (3 days old) is shown in Fig. 9.

Expression of pARP-EGFP was first observed 4 hours after injection at the 30%

epiboly stage. The timing of expression is similar to that of pCK-EGFP-injected embryos. However, unlike the pCK-EGFP transgenic embryos, the GFP expression under the ARP promoter occurred not only in the superficial layer of cells but also in deep layers of cells. In some batches of injected embryos, almost 100% of the injected embryos expressed initially. At later stages when some embryonic cells become overtly differentiated, it was found that the GFP expression occurred essentially in all different types of cells such as skin epithelia, muscle cells, lens, neural tissues, notochord, circulating blood cells and yolk cells (Fig. 10).

Under the MLC2f promoter, nearly 60% of the embryos expressed GFP. The earliest GFP expression started in trunk skeletal muscles about 19 hours after injection, which corresponds to the stage of 20-somite. Later, the GFP expression also occurred in head skeletal muscles including eye muscles, jaw muscles, gill muscles etc.

Transgenic founder zebrafish containing pMLC2f-EGFP emit a strong green fluorescent light under a blue or ultraviolet light (Fig. 11A). When the transgenic founders were crossed with wild-type fish, transgenic offspring were obtained that also displayed strong green fluorescence (Fig. 11B). The level of GFP expression is so high in the transgenic founders and offspring that green fluorescence can be observed when the fish are exposed to sunlight.

To identify the DNA elements conferring the strong promoter activity in skeletal muscles, deletion analysis of the 2-kb DNA fragment comprising the promoter was performed. Several deletion constructs, which contain 5' deletions of the MLC2f promoter upstream of the EGFP gene, were injected into the zebrafish embryos and the transient expression of GFP in early embryos (19-72 hpf) was compared. To facilitate the quantitative analysis of GFP expression, we define the level of expression as follows (Figs. 12A-12C):

Strong expression: GFP expression was detected in essentially 100% muscle fibers in the trunk.

Moderate expression: GFP expression was detected in several bundles of muscle fibers, usually in the mid-trunk region.

Weak expression: GFP expression occurred in dispersed muscle fibers and the number of GFP positive fibers is usually less than 20 per embryo.

As summarized in Fig. 13, deletion up to -283 bp maintained the GFP expression in skeletal muscles in 100% of the expressing embryos; however, the level of GFP expression from these deletion constructs varies greatly. Strong expression drops from

23% to 0% from the 2-kb (-2011 bp) promoter to the -283-bp promoter. Thus, only two constructs (-2011 bp and -1338 bp) are capable of maintaining the high level of expression and the highest expression was obtained only with the 2-kb promoter, indicating the importance of the promoter region of -1338 bp to -2011 bp for conferring the highest promoter activity.

The expression of GFP using pMLC2f-EGFP is much higher than that obtained using the pMCK-EGFP that contains a 1.5 kb of zebrafish *MCK* promoter. By the same assay in transient transgenic zebrafish embryos, only about 12% of the embryos injected with pMCK-EGFP expressed GFP. Among the expressing embryos, no strong expression was observed, and 70% and 30% showed moderate and weak expression, respectively. In comparison, about 60% of the embryos injected with pMLC2f-EGFP expressed GFP and 23%, 37% and 40% showed strong, moderate and weak expression, respectively.

Example IV: Potential applications of fluorescent transgenic fish

The fluorescent transgenic fish have use as ornamental fish in the market. Stably transgenic lines can be developed by breeding a GFP transgenic individual with a wild type fish or another transgenic fish. By isolation of more zebrafish gene promoters, such as eye-specific, bone-specific, tail-specific etc., and/or by classical breeding of these transgenic zebrafish, more varieties of fluorescent transgenic zebrafish can be produced. Previously, we have reported isolation of over 200 distinct zebrafish cDNA clones homologous to known genes (Gong et al., 1997). These isolated clones code for proteins in a variety of tissues and some of them are inducible by heat-shock, heavy metals, or hormones such as estrogens. By using the method of PCR amplification using gene-specific primers designed from the nucleotide sequences of these cDNAs, and the linker-specific primers described herein, the promoters of the genes represented by the cDNAs of Gong et al. can be used in the present invention. Thus, other tissue-specific promoters, hormone-inducible promoters, heavy-metal inducible promoters and the like from zebrafish can be isolated and used to make fluorescent zebrafish (or other fish species) that express a GFP or variant thereof, in response to the relevant compound.

Multiple color fluorescent fish may be generated by the same technique as blue fluorescent protein (BFP) gene, yellow fluorescent protein (YFP) gene and cyan fluorescent protein (CFP) gene are available from Clontech. For example, a transgenic fish with GFP under an eye-specific promoter, BFP under a skin-specific promoter, and YFP under a muscle-specific promoter will show the following multiple fluorescent colors: green eyes, blue skin and yellow muscle. By recombining different tissue specific promoters and fluorescent protein genes, more varieties of transgenic fish of different

fluorescent color patterns will be created. By expression of two or more different fluorescent proteins in the same tissue, an intermediate color may be created. For example, expression of both GFP and BFP under a skin-specific promoter, a dark-green skin color may be created.

5 By using a heavy metal- (such as cadmium, cobalt, chromium) inducible or hormone- (such as estrogen, androgen or other steroid hormone) inducible promoter, a biosensor system may be developed for monitoring environmental pollution and for evaluating water quality for human consumption and aquacultural uses. In such a biosensor system, the transgenic fish will glow with a green fluorescence (or other color depending
10 on the fluorescence protein gene used) when pollutants such as heavy metals and estrogens (or their derivatives) reach a threshold concentration in an aquatic environment. Such a biosensor system has advantages over classical analytical methods because it is rapid, visualizable, and capable of identifying specific compounds directly in complex mixture found in an aquatic environment, and is portable or less instrument dependent. Moreover,
15 the biosensor system also provides direct information on biotoxicity and it is biodegradable and regenerative.

Environmental monitoring of several substances can be accomplished by either creating one transgenic fish having genes encoding different colored fluorescent proteins driven by promoters responsive to each substance. Then the particular colors exhibited the
20 fish in an environment can be observed. Alternatively, a number of fish can be transformed with individual vectors, then the fish can be combined into a population for monitoring an environment and the colors expressed by each fish observed.

In addition, the fluorescent transgenic fish should also be valuable in the market for scientific research tools because they can be used for embryonic studies such as tracing cell
25 lineage and cell migration. Cells from transgenic fish expressing GFP can also be used as cellular and genetic markers in cell transplantation and nuclear transplantation experiments.

The chimeric gene constructs demonstrated successfully in zebrafish in the present invention should also be applicable to other fish species such as medaka, goldfish, carp
30 including koi, loach, tilapia, glassfish, catfish, angel fish, discus, eel, tetra, goby, gourami, guppy, Xiphophorus (swordtail), hatchet fish, Molly fish, pangasius, etc. The promoters described herein can be used directly in these fish species. Alternatively, the homologous gene promoters from other fish species can be isolated by the method described in this invention. For example, the isolated and characterized zebrafish cDNA clones and
35 promoters described in this invention can be used as molecular probes to screen for homologous promoters in other fish species by molecular hybridization or by PCR.

Alternatively, one can first isolate the zebrafish cDNA and promoters based on the sequences presented in SEQ ID NOS:1, 3, 5, 7, 8, 9, 20 and 22 or using data from other sequences of cDNAs disclosed by Gong et al. 1997, by PCR and then use the zebrafish gene fragments to obtain homologous genes from other fish species by the methods
5 mentioned above.

In addition, a strong muscle-specific promoter such as MLC2f is valuable to direct a gene to be expressed in muscle tissues for generation of other beneficial transgenic fish. For example, transgenic expression of a growth hormone gene under the muscle-specific promoter may stimulate somatic growth of transgenic fish. Such DNA can be introduced
10 either by microinjection, electroporation, or sperm carrier to generate germ-line transgenic fish, or by direct injection of naked DNA into skeletal muscles (Xu et al., 1999) or into other tissues or cavities, or by a biolistic method (gene bombardment or gene gun) (Gomez-Chiarri et al., 1996).

SEQUENCE LISTING

<110> GONG, Zhiyuan
 LAM, Toong Jin
 JU, Bensheng
 XU, Yanfei
 — HE, Jiangyan
 YAN, Tie

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Arg Leu Arg Leu Gln Lys Arg Gly Thr Gly Gly Val Asp Thr Ala Ser			
315	320	325	
gtt ggt gga gtg ttt gac att tcc aac gct gac cgt atc ggc tct tca			1120
Val Gly Gly Val Phe Asp Ile Ser Asn Ala Asp Arg Ile Gly Ser Ser			
330	335	340	345
gag gtt gag cag gtg cag tgt gtg gtt gat ggt gtc aag ctg atg gtg			1168
Glu Val Glu Gln Val Gln Cys Val Val Asp Gly Val Lys Leu Met Val			
350	355	360	
gag atg gag aag aag ctg gga gaa ggc cag tcc atc gac agc atg atc			1216
Glu Met Glu Lys Lys Leu Gly Glu Gly Gln Ser Ile Asp Ser Met Ile			
365	370	375	
cct gcc cag aag taa agcgggaggc ccttcattt ttttcttcgt ctttgtctgt			1271
Pro Ala Gln Lys			
380			
ttttttacag tccaacagca acgsagagga aaactgctgc tcaaaaagac agtctcacct			1331
ttgcacctgt cttcttttct ttttttccct tcttctctaa ttcccatgtc atttcgccat			1391
ctttttttcc actttgtttc ctattaagtc ggtaacatct tgggatcaga taccggsgc			1451
aggagtgagt gcttggttgc gaggcttcac ctcaatttca gccttggttg taaaaagtga			1511
atcaatcaaaa gttgtatttc aaaataaaaa tccccaataa aaaaaaaaaa aaaaaaaaaa			1571
aaaaaaaaaa aaaaaaaaaa			1589
<210> 4			
<211> 381			
<212> PRT			
<213> Danio rerio			
<400> 4			
Met Pro Phe Gly Asn Thr His Asn Asn Phe Lys Leu Asn Tyr Ser Val			

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1	5	10	15
Asp Glu Glu Tyr	Pro Asp Leu Ser	Lys His Asn Asn His	Met Ala Lys
20		25	30
Val Leu Thr Lys	Glu Met Tyr Gly	Lys Leu Arg Asp	Lys Gln Thr Pro
35		40	45
Pro Gly Phe Thr	Val Asp Asp Val	Ile Gln Thr Gly	Val Asp Asn Pro
50		55	60
Gly His Pro Phe	Ile Met Thr Val	Gly Cys Val Ala	Gly Asp Glu Glu
65		70	75
80			
Ser Tyr Asp Val	Phe Lys Asp Leu	Phe Asp Pro Val	Ile Ser Asp Arg
85		90	95
His Gly Gly Tyr	Lys Ala Thr Asp	Lys His Lys Thr	Asp Leu Asn Phe
100		105	110
Glu Asn Leu Lys	Gly Gly Asp Asp	Leu Asp Pro Asn	Tyr Phe Leu Ser
115		120	125
Ser Arg Val Arg	Thr Gly Arg Ser	Ile Lys Gly Tyr	Pro Leu Pro Pro
130		135	140
His Asn Ser Arg	Gly Glu Arg Arg	Ala Val Glu Lys	Leu Ser Val Glu
145		150	155
160			
Ala Leu Ser Ser	Leu Asp Gly Glu	Phe Lys Gly Lys	Tyr Tyr Pro Leu
165		170	175
Lys Ser Met Thr	Asp Asp Glu Gln	Glu Gln Leu Ile	Ala Asp His Phe
180		185	190
Leu Phe Asp Lys	Pro Val Ser Pro	Leu Leu Leu Ala	Ala Gly Met Ala
195		200	205
Arg Asp Trp Pro	Asp Ala Arg Gly	Ile Trp His Asn	Glu Asn Lys Ala
210		215	220
Phe Leu Val Trp	Val Lys Gln Glu	Asp His Leu Arg	Val Ile Ser Met
225		230	235
240			
Gln Lys Gly Gly	Asn Met Lys Glu	Val Phe Lys Arg	Phe Cys Val Gly
245		250	255
Leu Gln Arg Ile	Glu Glu Ile Phe	Lys Lys His Asn	His Gly Phe Met
260		265	270
Trp Asn Glu His	Leu Gly Phe Val	Leu Thr Cys Pro	Ser Asn Leu Gly
275		280	285
Thr Gly Leu Arg	Gly Gly Val His	Val Lys Leu Pro	Lys Leu Ser Thr
290		295	300
His Ala Lys Phe	Glu Glu Ile Leu	Thr Arg Leu Arg	Leu Gln Lys Arg
305		310	315
320			
Gly Thr Gly Gly	Val Asp Thr Ala	Ser Val Gly Gly	Val Phe Asp Ile
325		330	335
Ser Asn Ala Asp	Arg Ile Gly Ser	Ser Glu Val Glu	Gln Val Gln Cys
340		345	350

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Val Val Asp Gly Val Lys Leu Met Val Glu Met Glu Lys Lys Leu Gly
 355 360 365

Glu Gly Gln Ser Ile Asp Ser Met Ile Pro Ala Gln Lys
 370 375 380

<210> 5
 <211> 1104
 <212> DNA
 <213> Danio rerio

<220>
 <221> CDS
 <222> (75)..(1034)

<220>
 <221> primer_bind
 <222> (45)..(64)
 <223> ARP2

<220>
 <221> primer_bind
 <222> (87)..(112)
 <223> ARP1

<220>
 <221> polyA_signal
 <222> (1069)..(1074)

<400> 5
 cgcgtcccta ccgtgagatt ttacaacctt gtctttaaac cggtctgtca ccgataccttg 60
 gaagcactgc aaag atg ccc agg gaa gac agg gcc acg tgg aag tcc aac 110
 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn
 1 5 10
 tat ttt ctg aaa atc atc caa ctg ctg gat gac ttc ccc aag tgt ttc 158
 Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe
 15 20 25
 atc gtg ggc gca gac aat gtc ggc tcc aag cag atg cag acc atc cgt 206
 Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg
 30 35 40
 ctg tcc ctg cgg ggc aag gcc gtc gtg ctc atg ggg aaa aac acc atg 254
 Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met
 45 50 55 60
 atg agg aag gcc att cgt ggc cac ctg gaa aac aac cca gct ctg gag 302
 Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu
 65 70 75
 agg ctg ctt ccc cac atc cgc ggg aac gtg ggc ttc gtc ttc acc aag 350
 Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys
 80 85 90
 gag gat ctg act gag gtc cga gac ctg ctg ctg gca aac aaa gtg ccc 398
 Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro
 95 100 105
 gct gct gcc cgt gct ggt gcc atc gcc ccc tgt gag gtg act gtg ccg 446
 Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro
 110 115 120
 gcc cag aac acc ggg ctc ggt cct gag aag acc tct ttc ttc cag gct 494

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Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala
 125 130 135 140

ttg gga atc acc acc aag atc tcc aga gga acc att gaa atc ttg agt 542
 Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser
 145 150 155

gac gtt cag ctt atc aaa cct gga gac aag gtg ggc gcc agc gag gcc 590
 Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala
 160 165 170

acg ctg ctg aac atg ctg aac atg ctg aac atc tcg ccc ttc tcc tac 638
 Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr
 175 180 185

ggg ctg atc atc cag cag gtg tat gat aac ggc agt gtc tac agc ccc 686
 Gly Leu Ile Ile Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro
 190 195 200

gag gtg ctg gac atc act gag gac gcc ctg cac aag agg ttc ctg aag 734
 Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys
 205 210 215 220

ggt gtg agg aac atc gcc agt gtg tgt ctg cag atc ggc tac cca act 782
 Gly Val Arg Asn Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr
 225 230 235

ctt gct tcc atc cct cac act atc atc aat gga tac aag agg gtc ctg 830
 Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu
 240 245 250

gct gtc act gtc gaa aca gac tac aca ttc ccc ttg gct gag aag gtg 878
 Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val
 255 260 265

aag gcc tac ctg gct gat ccc acc gct ttc gct gtt gca gcc cct gtt 926
 Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val
 270 275 280

gcg gca gct aca gag cag aaa tcc gct gct cct gcg gct aaa gag gag 974
 Ala Ala Ala Thr Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu
 285 290 295 300

gca ccc aag gag gat tct gag gag tct gat gaa gac atg ggc ttc ggc 1022
 Ala Pro Lys Glu Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly
 305 310 315

ctg ttt gat taa accagacacc gaatatccat gtctgttttaa catcaataaa 1074
 Leu Phe Asp 320

acatctggaa acaaaaaaaaaa aaaaaaaaaa 1104

<210> 6
 <211> 319
 <212> PRT
 <213> Danio rerio

<400> 6
 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys
 1 5 10 15
 Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe Ile Val Gly Ala
 20 25 30

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Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg Leu Ser Leu Arg
 35 40 45
 Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala
 50 55 60
 Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro
 65 70 75 80
 His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr
 85 90 95
 Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg
 100 105 110
 Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr
 115 120 125
 Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr
 130 135 140
 Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu
 145 150 155 160
 Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn
 165 170 175
 Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile
 180 185 190
 Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp
 195 200 205
 Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn
 210 215 220
 Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile
 225 230 235 240
 Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val
 245 250 255
 Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu
 260 265 270
 Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr
 275 280 285
 Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu
 290 295 300
 Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
 305 310 315

<210> 7

<211> 2241

<212> DNA

<213> Danio rerio

<220>

<221> TATA signal

<222> (2103)..(2108)

<220>
<221> primer_bind
<222> (2221)..(2241)
<223> CK2

<220>
<221> misc_feature
<222> (2142)..(2235)
<223> Identical to the 5' CK cDNA

<400> 7
ccttccttc tacttttgac gtccttttaa gagcttgtgc atgaaagcag atttgagact 60
gattactcat ctcaaacc cacaacagg gatgattgcc gtaccatgat ctcacacctt 120
tcacacctgg ttatactat gatagttgta gacgattgcg taatgctatt aaatgcccat 180
cagtgtggc tgtgacccc aactgctgcc atttcgtgtt gacttgacg agaaatgaga 240
aattgtctga ctatgcaggg tgcctatgcg tgggaacatt tatcagtggc cattaaatac 300
tatagtttac agttagacca aagtgtgctg tatttttgtg ttagcttagc tgcagttttt 360
gtgtgtgaag taacaaatga caaatactca aactattgta attaagtagt tttctcaga 420
aattgtaatt tactaagtag tttaaaaatg tgtactttta ctttccttg agtacatttt 480
tagtgcagtg ttggtacttt tatttcactt ctttccttca acctgcagtc actactttat 540
ttattcttgt ctatgtggat tagacaaatc agtctgtga ttctgttcca atcaaattgc 600
acatagaagg taaatcacat cataatgaac taccttaaga catgggccat ttataattgc 660
agcaaactgt ttgccagcat taaaagaaga tgtcaaaaat atttacacgc attaacccag 720
agactgctta gatgcatgac actgatgaga agatgatgga tgtttactgt atgatgaccg 780
aaataacttt aaacgcacac aagacggcac aagacgtcaa catggcggtta ggttgacgtt 840
gtaccccaac gcagtgggga cgttgcatth tgtttagaaa tgaaaattag gttgacgtca 900
gaactcaacg tcaggtcgat gtcaatgttc aacatccaat ctaaaatcat atatcaatgt 960
ctaatgatgt tacagcttga tgttatgcgg atgttacctc tatgacgtct atcagacgtt 1020
ggattatggt tgccatacct gatgaataaa tgctattatt tgacgttggc ttaagatgtt 1080
ggttcgacat tggattttgg tcgctttcca acacaacct aatccacca atattaactt 1140
cctatgacat cgttattgga cgtcaaaata acaatatact tagatgctgg ctgacttttg 1200
aatttaggtc accacaacct atatttaacc taatattaac atcttatgat gttgtgtgcc 1260
tgctgggcaa taactaaatg cactacagaa tgttacgttt acacacatgt aaattacatg 1320
taaatgcac agcttttcac agcataatac tcactactta ctactcttga gtacttttaa 1380
aaaagctact ttctactcat actttgagta atatttaca ctgatacttt tactcgact 1440
acatttttag gcatgtattg atatttttac tatgattttt cagtactctt tccactactg 1500
cagccctccc catacataat cgtatgttta cacatatggt ggagtttaga gccataatct 1560
acattagctt tgttagccgc tagcattact gtgcagaatt gtgtgtgtgc acattttcca 1620

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atatcaatac agaaggaaac tgtgttccct gttcccttgt aaatctcaac aatgcaactg 1680
 ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaag tgaatggaaa 1740
 aaagcctttc attaatgtga aagtgtgtgc gcgccccacc cagataaaaa gagcagaggt 1800
 taacatgttc tctacggctg tccagccaac cagatactga ggcagaaaca caccgctgg 1860
 cagatggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtctcaagt 1920
 ctcaagcctc tccttgcaat ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
 caacatttat ctaccactt tctctctgta cctgtctaac aggtagggtg tgtgtgagag 2040
 tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtca gctccaccct ctcaagagtg 2100
 tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
 tgagcaacct cctccactca ctctctctc agagagcact ctgtacctc cttctcagca 2220
 actcaaagac acaggatccg g 2241

<210> 8
 <211> 1456
 <212> DNA
 <213> Danio rerio

<220>
 <221> TATA_signal
 <222> (1389)..(1394)

<220>
 <221> primer_bind
 <222> (1433)..(1456)
 <223> MCK2

<220>
 <221> misc_feature
 <222> (1428)..(1453)
 <223> Identical to the 5' MCK cDNA

<400> 8
 gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
 tgtggcttaa tcttggtga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
 gcatgtgcac catgacaggc ctgttattca cacttggtgc catgttgag actgttcggc 180
 cagctatagt tttcttcaca gagtctggg tcacctaatg tcacaaggaa gaaacatgtt 240
 acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
 ttacagctta aaagattgct agacagaaaa accaggagg ggttttccca taatatccag 360
 tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
 gtgacagaaa accagagatg gaaatacctt cttttgaatt gcataattgc taaaagaag 480
 acacaacagg gatagttcac ccaaaaaaca gaccattctt ttttctgtt gaacaaaaat 540
 taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
 aagtcaatgg gtcttcagc attttttcaa tataccttac ttgagttca aaagaaaaac 660

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acatctcaaa taggtttgag gttgaataaa cttttttcat tttggggtgg actatcccta 720
attatttgac acttaagatt tatagtaaatt ctttttatag actttctccc cttattaaac 780
atgggtgaat ttatcttcat gtttatgtct ggggtgtgct tttttgaaaa gattttccctg 840
tcaaagtgtt ttgtgtatgg ttggcgacac atagactgaa ctggcctatc acacagaactt 900
tcataacaac tccagttgat gccctttcac cctcagtga taaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaatt gagtttgcac 1020
ccagaatcat gtgggtgaacg aagcctacca agagattttt gaaagccatc ggctgacac 1080
gcgcaacttct gatatctgtg gtatgttttg caaaagtgtc gctcagcctt tttagcatgg 1140
cagatccctcc acatcccac acccctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccacac gctgccacct 1260
catctaggat gcctggggcc taaattgaag cttttcttac actaaacagg gcataagaga 1320
ccagcgccag ccaatcataa ttcagtgcac tctaaaatgg gccagccaat ggctgcaggg 1380
gctagaggta tatatatcca aatcaaactc ttcttgcttg ggtgacctt atttcggctt 1440
ggtgaacagg atccgg 1456

<210> 9
<211> 2205
<212> DNA
<213> Danio rerio

<220>
<221> primer_bind
<222> (2179)..(2205)
<223> ARP2

<220>
<221> misc_feature
<222> (2153)..(2199)
<223> Identical to the 5' ARP cDNA

<220>
<221> intron
<222> (792)..(2152)

<220>
<221> misc_feature
<222> (775)..(791)
<223> Identical to the 5' ARP cDNA

<400> 9
atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgac 60
attttaattt gtgttgtata attttacatt ttgtaagtat tttttttata aaaaatatat 120
agaaataata caaatttggt tacagtattc ttagttattg caataaacga attttatata 180
gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300
agataataaa gtgacttttt tgggcggacc aaatttccct attaatggtc aattcattaa 360

aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
gtgcagatTT ttggctgttg ttagaaggga tacatctgcg gccgaaagtt aacgggaact 480
atttacattc tttgctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540
tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaatgatgc 600
tatattgacc gcagctgtat cttttctaag tgcgactgta caaatacgca ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgcaca gatacgcat ttcgcgcga ttctgattgg 720
atgatcgact gatactaata ttgtgccgt tcttttcgcg gctctttct ttcacgcgtc 780
cctaccgtga ggtaaggctg acgccgtct tgtggcggt tcttaaaatg tgtaataaaa 840
taacatcata agaggtcacg agaaggtcta cgtgtgttta atatcagcgg cggttattat 900
tatgcgttta aagcttgtgt aatgattttt acagtaaaag ttagcactag cctgttagca 960
caggcctcgt gcgccatgtg tgacgcgacg ttttaatagc atcttatttg attttgatga 1020
tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080
ttacatgcta gtacttgtgc tagtcggtcg atccacattg agatgttgcg ctatttgcca 1140
ttttaaaacc agttactctc attttagtga aatattctta agccactaag ttaaaatttg 1200
tcaatcacat ataattgtgt ttatgtttta tttgagtcac cataccaggt aatagtttta 1260
tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320
gtaaagttaa tcttaagggt gtaaaggctc acccaaaaaga caattcaccg tcaagtgttt 1380
tcaaactctta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440
accataatac aaatacagga aaaatatact atagaagtcg atggttacag gttttctgca 1500
ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaagggt 1560
tgcataaatc agttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620
gcagtggta ccaagcttgt tctgaagggt ccagtgtcct acagatttta gctccaacct 1680
taattaaaca cacctgaaca agctaataca ggtcttacta ggtatgtttg aaacatccag 1740
gcaggtgtgt tgatgcaaga tagagctaaa ccctgcagggt acaatggccc aacaggattg 1800
gtgaccctcg cctcaagcca tcacaaatgc attatggtat taagaaatgt gcaggttcag 1860
ttatggacag gctgttgacg tgcttggtcg tegtccac tgcacaaatg aacatgattc 1920
cttctatccc tgtctgtctg catctcatga cttgcaggga cgtgtgtctc agacacgttt 1980
atagcagtaa atcaaataca atagtgtctt gattatcttt aaatatattga aagcttataa 2040
taggcaacca aattacctgg aaacagttta caaacagtaa ttcataattt gtcatttaaat 2100
aagatgcaca caaggcaggt gtaaaagtat tgcttggtgt tgtaatcctc agattttaca 2160
accttgcttt taaaccggct gttcaccgat ccttggaagg gatcc 2205

<210> 10

<211> 24

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin
— gene specific primer

<400> 10
cgctggagta agagatagac ctgg

24

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin
gene specific primer

<220>
<221> misc_feature
<222> (1)..(6)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 11
ccggatcctg tgtctttgag ttgctg

26

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 12
ccggatcctt gggatcagat cctg

24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (1)..(3)
<223> Introduced for restriction site

<220>
<221> misc_feature

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<222> (3)..(8)
<223> BamHI site

<400> 13
ccggatcctg ttcaccaagc cgaa

24

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<400> 14
tagttggact tccacgtgcc ctgtc

25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<220>
<221> misc_feature
<222> (1)..(7)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI site

<400> 15
ggatcccttc caaggatcgg tgaaca

26

<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

<400> 16
gttcacatctt acaagctagc gctgaacaat gctgtggaca agcttgaatt c

51

<210> 17
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

<220>

<223> n is a dideoxycytidine

<400> 17
gaattcaagn

10

<210> 18

<211> 21

<212> DNA

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The following references, referred to in this application, are hereby incorporated by reference in their entirety.

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CLAIMS

1. A zebrafish cytokeratin gene promoter which is capable of directing a structural gene to be predominantly expressed in skin epithelia when it is inserted in front of the structural gene and introduced into fish embryos.
2. A zebrafish muscle creatine kinase gene promoter which is capable of directing a structural gene to be specifically expressed in muscles when it is inserted in front of the structural gene and introduced into fish embryos.
3. A zebrafish fast skeletal muscle isoform of myosin light chain 2 gene promoter which is capable of directing a structural gene to be predominantly expressed in skeletal muscles when it is inserted in front of the structural gene and introduced into fish embryos.
4. A zebrafish acidic ribosomal protein P0 gene promoter which is capable of directing a structural gene to be expressed ubiquitously in all tissues when it is inserted in front of the structural gene and introduced into fish embryos.
5. A recombinant DNA molecule comprising a structural gene and the promoter of claim 1, 2, 3 or 4 arranged upstream of said structural gene.
6. A chimeric gene comprising the promoter of claim 1, 2, 3 or 4, operatively linked to DNA encoding a protein selected from the group consisting of GFP, modified GFP, EGFP, BFP, EBFP, YFP, EYFP, CFP, ECFP, luciferase, β -galactosidase, chloramphenicol acetyltransferase, and growth hormone.
7. A transgenic fish comprising a chimeric gene comprising the promoter of claim 1, 2, 3 or 4.
8. The transgenic fish of claim 7, which contains said promoter in germ cells and/or in somatic cells and which is capable of breeding with either a said transgenic fish or a non-transgenic fish to produce viable and fertile transgenic progeny.
9. The transgenic fish of claim 7, and progeny of said fish that emits green fluorescence when the whole fish is exposed to a blue or ultraviolet light.
10. A transgenic fish comprising a DNA that encodes a fluorescent protein under control of a promoter that causes said DNA (1) to be expressed in predominately

skin epithelia, (2) to be specifically expressed in muscles, (3) to be predominantly expressed in skeletal muscles, or (4) to be expressed ubiquitously in all tissues.

— 11. The transgenic fish of claim 8, wherein said fluorescent protein is expressed a level sufficient that said fish fluoresces upon exposure to sunlight or daylight.

5 12. The transgenic fish of claim 11, wherein said high expression is induced by exposure of said fish to a steroid compound or to a heavy metal.

13. The transgenic fish of claim 10, wherein said promoter is a promoter which naturally occurs in the genome of a fish of the same species as the transgenic fish.

10 14. A recombinant DNA vector comprising a promoter DNA that hybridizes under stringent conditions to a polynucleotide of any one of SEQ ID NOS:7, 8, 9, or 22, operatively linked to a structural gene encoding a fluorescent or chemiluminescent protein.

15. A cell transformed with the vector of claim 14.

15 16. A transgenic fish comprising a chimeric gene in turn comprising a promoter DNA that hybridizes under stringent conditions to a polynucleotide of any one of SEQ ID NOS:7, 8, 9, or 22, operatively linked to a structural gene encoding a fluorescent or a chemiluminescent protein.

17. A method for sensing a steroid hormone or a steroid hormone derivative in a water sample comprising:

20 (a) contacting a fish expressing a fluorescent or chemiluminescent protein under control of an estrogen- or other steroid hormone-inducible promoter with a sample of water; and
(b) measuring the amount of fluorescent or chemiluminescent light from said fish.

25 18. A method for sensing heavy metals, such as zinc, copper, cadmium, mercury etc., in a water sample comprising:

(a) contacting a fish expressing a fluorescent or chemiluminescent protein under control of a heavy metal-inducible promoter with a sample of water; and
(b) measuring the amount of fluorescent or chemiluminescent light from said fish.

Abstract of the Disclosure

Four zebrafish gene promoters, which are skin specific, muscle specific, skeletal muscle specific and ubiquitously expressed, respectively, were isolated and ligated to the 5' end of the EGFP gene. When the resulting chimeric gene constructs were introduced into zebrafish, the transgenic zebrafish emit green fluorescence under a blue light or ultra-violet light according to the specificity of the promoters used. Thus, new varieties of ornamental fish of different fluorescence patters, e.g., skin fluorescence, muscle fluorescence, skeletal muscle-specific and/or ubiquitous fluorescence, are developed.

Fig. 1A

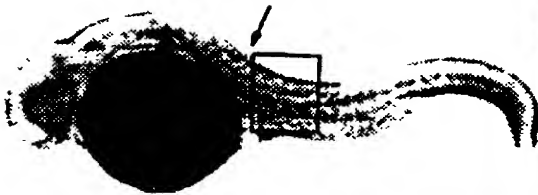


Fig. 1B

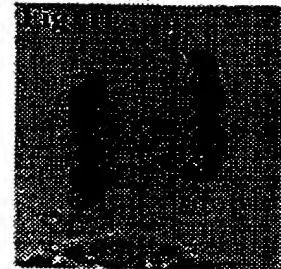
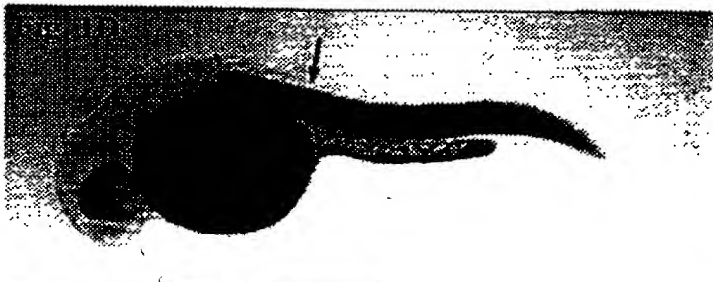
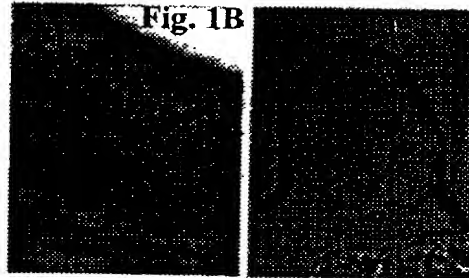




Fig. 1H



Fig. 1I

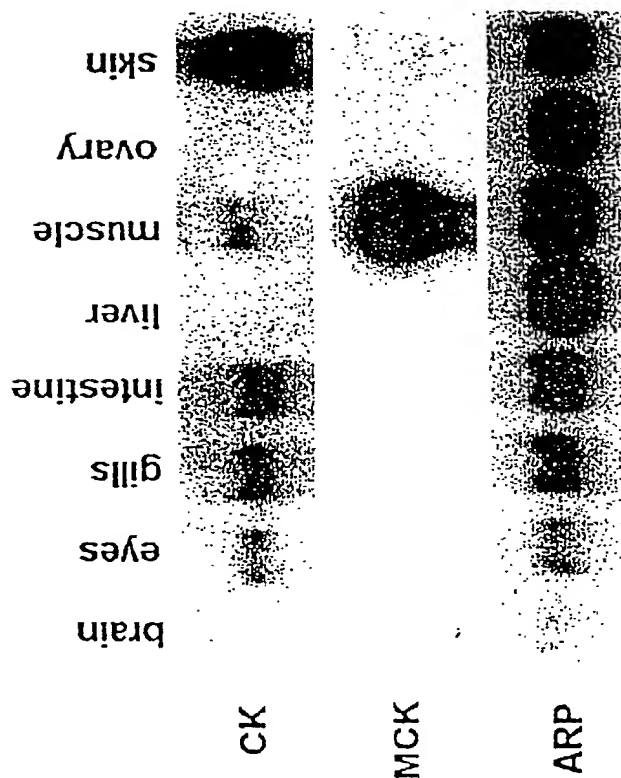


Fig. 2A

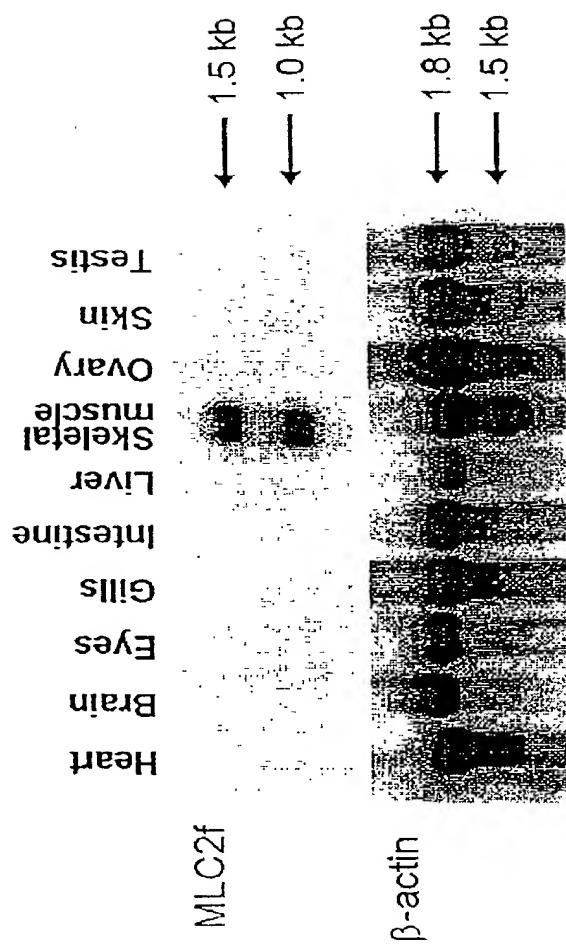


Fig. 2B

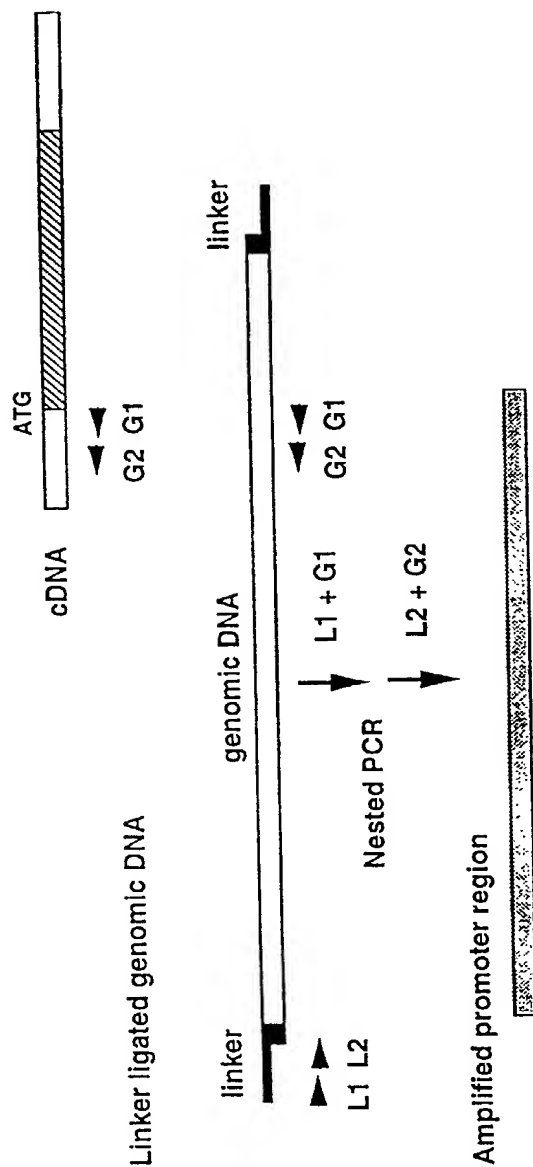


Fig. 3

09/913898

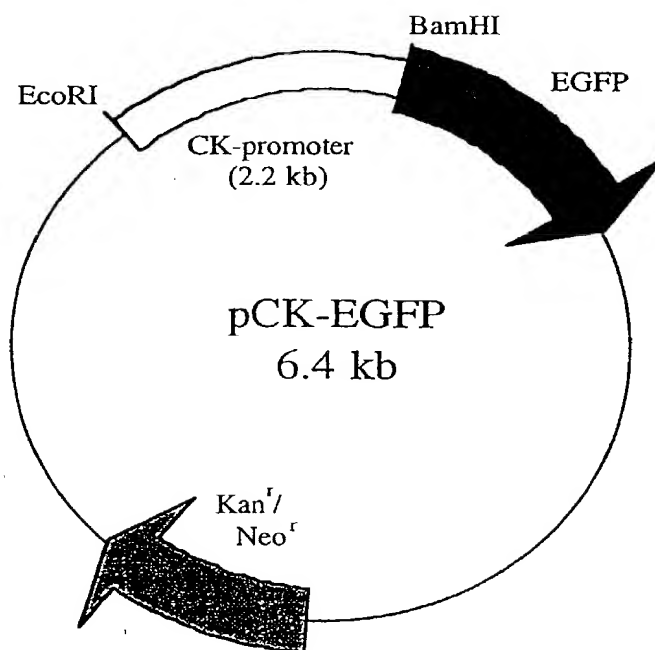


Fig. 4

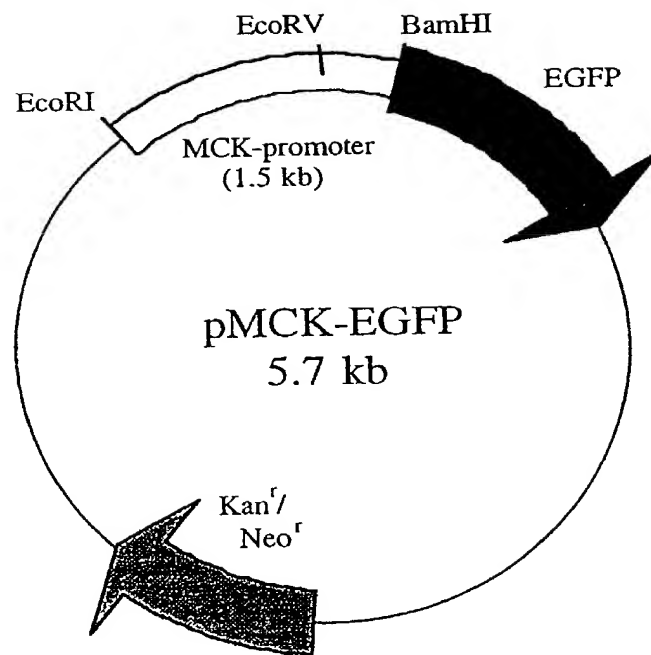


Fig. 5

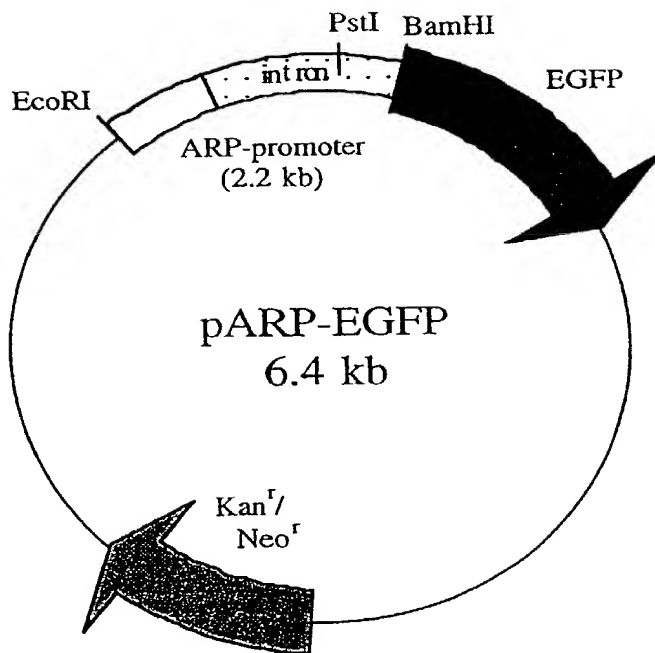


Fig. 6

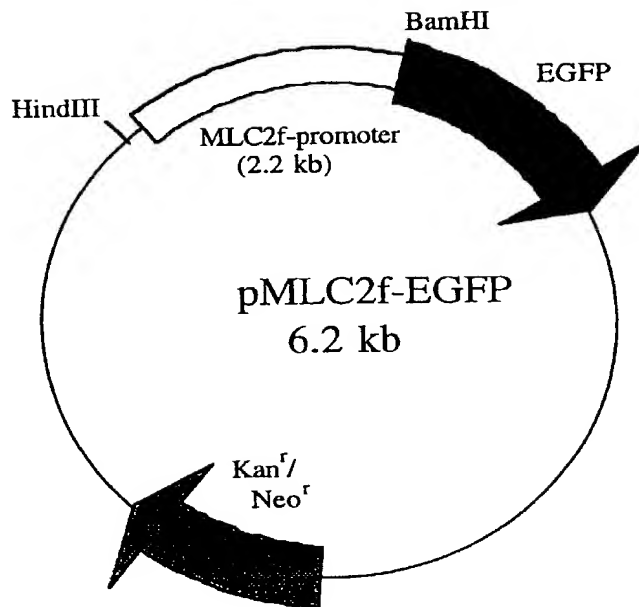


Fig. 7

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PCT/SG99/00079

- 10/15 -

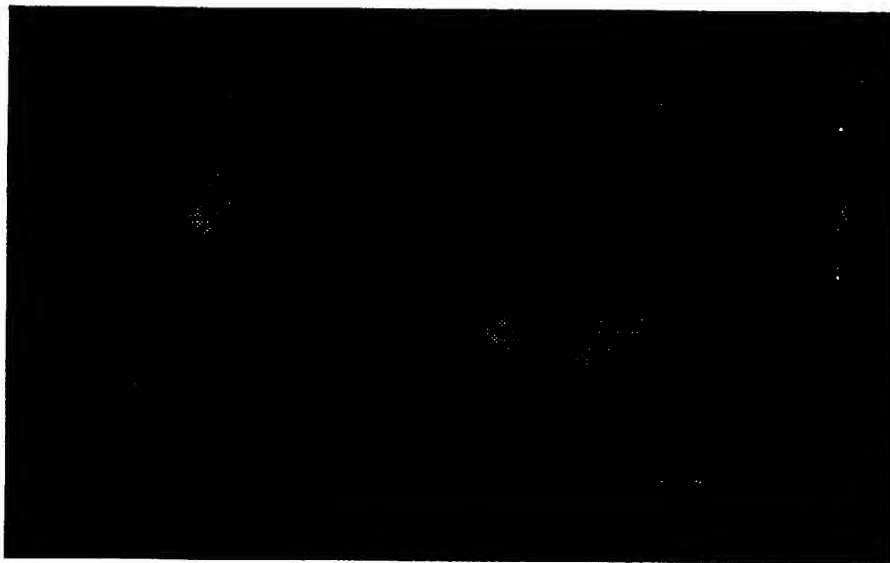


Fig. 8

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- 11/15 -

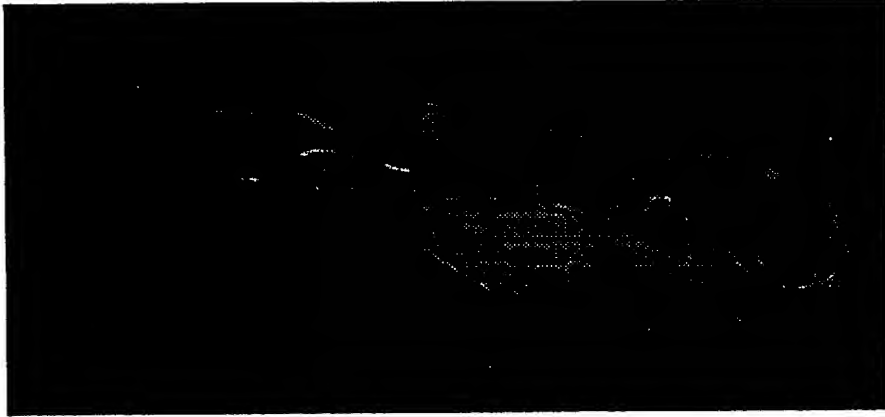


Fig. 9

SUBSTITUTE SHEET (RULE 26)

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- 12/15 -



Fig. 10

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- 13/15 -



Fig. 11A



Fig. 11B

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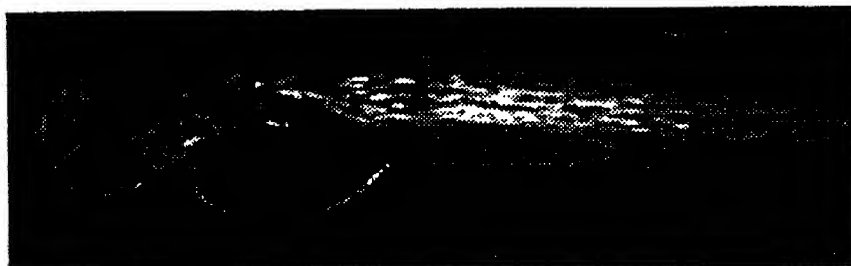


Fig. 12A

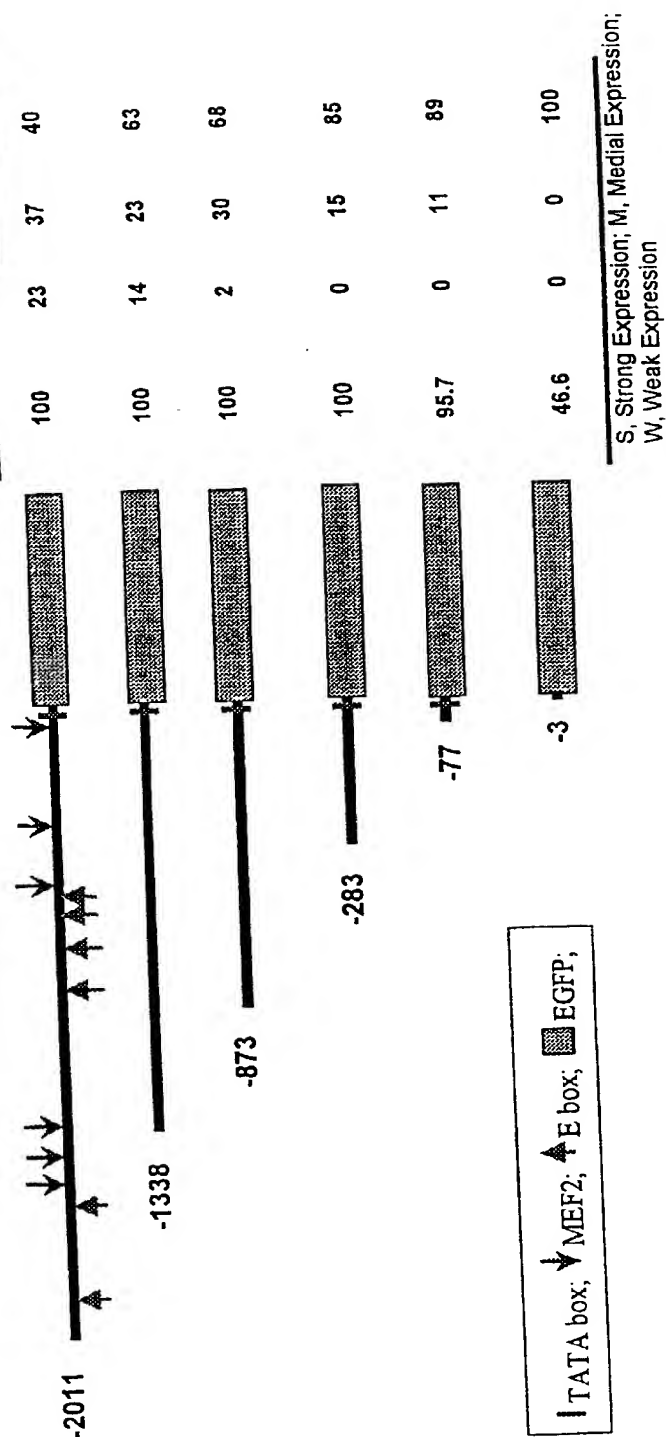


Fig. 12B



Fig. 12C

Fig. 13



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and amended on _____ (if applicable) and/or
the specification was filed on July 16, 1999 as PCT
International Application Number PCT/SG99/00079; and was
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I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

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Priority Claimed

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<u>9903367-2</u> (Number)	<u>Singapore</u> (Country)	<u>July 14, 1999</u> (Month/Day/Year Filed)	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
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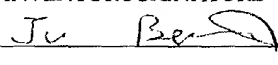
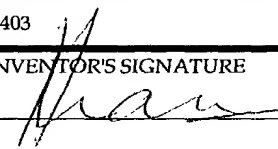
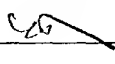
Full Name of Third
Inventor, if any:
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Full Name of Fourth
Inventor, if any:
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Full Name of Fifth
Inventor, if any:
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Inventor, if any:
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MAILING ADDRESS (Complete Street Address including City, State & Country) <u>2636 North Moreland Blvd., Apt. 8, Cleveland, OH 44120, USA</u>		
GIVEN NAME/FAMILY NAME <u>Bensheng JU</u>	INVENTOR'S SIGNATURE 	DATE* <u>08/08/2001</u>
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GIVEN NAME/FAMILY NAME <u>Toong Jin LAM</u>	INVENTOR'S SIGNATURE 	DATE* <u>08/08/2001</u>
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GIVEN NAME/FAMILY NAME Bensheng JU	INVENTOR'S SIGNATURE	DATE*
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GIVEN NAME/FAMILY NAME Toong Jin LAM	INVENTOR'S SIGNATURE	DATE*
Residence (City, State & Country) Singapore, Singapore	CITIZENSHIP Singapore	
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GIVEN NAME/FAMILY NAME Yanfei XU	INVENTOR'S SIGNATURE <i>[Signature]</i>	DATE* 8/18/01
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GIVEN NAME/FAMILY NAME Tie YAN	INVENTOR'S SIGNATURE	DATE*
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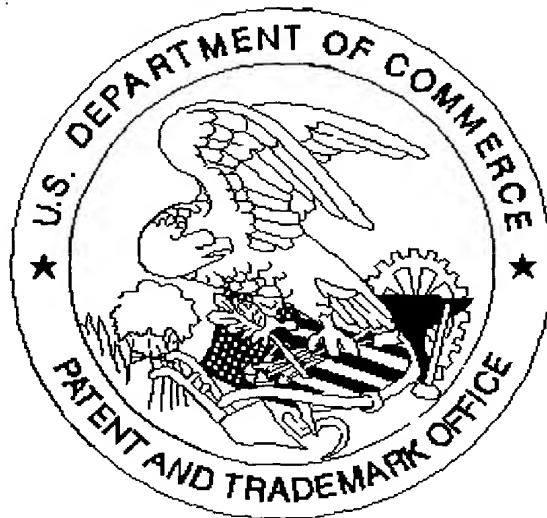
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